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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AL104547 AL2332721 AL233281 AL233281 AL233281 AL233281 AL134656 AL0488773 AL154070 AL055548 AA065542 AA055548 AA06542 AA0798652 AA079863 AA178891 AA18433 AA450933 AA73968 AA239639 AL276269 AA1786176 AA0758514 AA83417 AA0758514 AA83417 AA178616 AA1786176 AA1786176 AA18433 AA176292 AA176202 A	Ore Match Length DB ID 5.6 54.1 602 43 Al104547 6.6 54.1 602 43 Al104547 6.6 54.1 602 43 Al104547 6.6 54.1 602 45 Al232721 6.6 54.1 482 41 Al24887 34.9 34.9 456 42 Al136965 6.6 34.2 482 41 Al24887 352 32.9 454 42 Al154070 4.4 20.8 33.9 444 27 Al154070 4.4 20.8 34.2 444 27 Al154070 5.6 27.0 569 37 A802564 7.4 20.9 540 40 AN085581 4.2 21.3 446 27 AR05581 4.4 21.3 260 30 AA239639 4.2 22.1 574 36 AR05931 6.6 22.0 374 33 AA45093 6.6 22.1 574 36 AR05581 4.4 21.3 260 30 AA239639 4.4 21.3 260 30 AA239639 4.4 21.3 260 37 A802551 4.4 21.3 260 37 A802551 4.4 21.3 30 32 AA379908 4.4 19.5 337 81 AR045467 6.6 17.3 44 413 42 Al1762612 4.6 15.0 431 43 Al18912 6.6 14.3 31 34 AR059368 8.4 13.5 447 39 AR864952 6.6 14.3 31 447 45 Al176292 8.6 14.3 31 34 AR06176 6.6 17.3 40 AR06176 6.6 17.3 41 41 41 41 41 41 41 41 41 41 41 41 41	Descriptio	A1104547 A1232721 A1233681	AA034568 AI136965	AI048873 AA032667	AI154070 AW434638	AQ055548	W83837 mf	C77953 C7 AA450933	C78711 C7	AQ798652	AA029831 AA780068	AA239639	A11/8891 AA067980	AW005581 AW418433	AI871472	AU045080	AUU4546U W86176 zh	AI578514 W93417 2d	AA836105 AT240670	A12408/3 A1276262	AI076231 AW261921	AI189612 AA379908	M926/2 ZI AA464962	AA85/959 AI200129	K20463 yg W86177 zh	7670/674			E- U Li	Bento Soares Rattus sp.				mirata, vertebrata; ; Muridae; Murinae;	, Mason, T.M.,	of a Rat EST	
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"ATCC (inhost):2025533"
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Sciurognathi; Muridae; Murinae; Rattus.
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Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 680)

Lee, N. H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,

Kerlavage, A.R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (REST) Catalog &
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Unpublished (1998)
On Oct 30, 1998 this sequence version replaced gi:3816601.
Other_ESTs: TC60009
Contact: Lee, NH
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                                                                                                                                                                                                                                                                                                                                                                                           Length 680;
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                                                                                                                                                                                     The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tlgr.org Seq primer: M13-21.
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200 TTGGAAGGCTGAGGCTGGAGAATGGGAAGTGTAAGCTGGGCCTGGCTTTCATAGTGAGGC 141
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Rerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818 tactgtgggtgctgaagctggtaccagaacacagcccccactggtgatgagcccaactc
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Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:2044369.
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, Tel: (301)-838-3529 Fax: (301)-838-0206 Email: nhiee@tigr.org Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                     AI233681 462 bp mRNA EST
EST2203099 Normalized rat Kidney, Bento Soares
RKID181 3' end, mRNA sequence.
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40.6%; Score 446.6; DB 43;
Best Local Similarity 99.1%; Pred. No. 2.9e-115;
Matches 449; Conservative 0; Mismatches 4; 1
                                                                              | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 1090 | 
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RESULT 5
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:280660
                                                                                                                                                AA034568 456 bp mRNA EST 23-AUG-1996 m149all.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:466844 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1966)
On Nov 29, 1993 this sequence version replaced gi:634431.
Contact: Maran MyMouse EST project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="TMAGE:466844"
/clone=11b="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 421.
Location/Qualifiers
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/strain="C57BL/6J"
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Gaps

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Length 456;

34.9%; Score 383.4; DB 27; Length llarity 91.8%; Pred. No. 1.8e-97; Conservative 0; Mismatches 36; Indels

al Similarity 405; Conserv

Query Match Best Local Matches 40

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On Jan 19, 1998 this sequence version replaced g1:2150747.

On Jan 19, 1998 this sequence version replaced g1:2150747.

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8250
Fax: 319 335 9565
Email: msoaresekblue.weeg.uiowa.edu
The sequence tag present in the CDNA between the Not! site and the oligo-dT track served to identify it as a clone from the normalized adult Spleen library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I. M. A.G.E.
CONSORTIUM at LIME (info@image.llnl.gov). IMAGE ID=1787109 The following repetitive elements were found in this cDNA sequence: 33-145, >PBLD7#SINE_Alu
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 386)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                 atgcaactgtggttaggaccttctcttcggactggtcaagaaacgggaagaaagggatgtc 136
                                                                                               376
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18 CDNA clone
                                             cttagacaggagcaccttcagaaagttgttgaaacttgtagtcggggccctgcatgggaa
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UI-R-C2p-nz-d-10-0-DI.sl UI-R-C2p Rattus norvegicus
UI-R-C2p-nz-d-10-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
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Rattus norvegicus
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Marra,M., Hillier,L.; Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Smeptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 tttgtaatgcaactgtggttaggaccttctcttcggactggtcaagaaacgggaagaag 130
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                                                                     Eukaryota; Metazoq; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Mus.
1 (bases 1 to 482)
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                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
On Jan 14, 1998 this sequence version replaced gi:1798596.
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano mouse liver mlia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"/strain="C57BL"
                                                                                                                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
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High quality sequence stop: 463.
Location/Qualifiers
1 .482
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/clone="IMAGE:1431579"
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/lab_host="DH10B"
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Jouse mouse.
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                                                                                                                       /dev_stage="bH108 (life Technologies)"
/dab_host="bH108 (life Technologies)"
/dote="vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: ECO RI; THe UI-R-C2p
library is a subtracted library derived from the UI-R-C0 library.
UI-R-C0 library are UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified coNa inserts from
UI-R-C1 clones from which 3: ESTS had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2P library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-805, 1996, 1996)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1015 ggaagtgtaagctgggcctggctttcatagtgaggctcagtgtcgaattaaagaggtaaa 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uc76f0.71 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1431579 5', mRNA sequence.
AIO48873 GI:3297160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775 agaagaagtgtgagcgcaaactgcaggactgactgaaccctggtactgtgggtgctgaag 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgagaacgtattttaagtgaaaagacagcgggactttcaggttttgttttattgagtcaac 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 TGAGAACGTATTTTAAGTGAAAAGACAGCGGGACTTTCAGGTTTTGTTTTATGAGTCAAC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             715 ccaaatttcaggagctgcggtacagtgtagccttggtccttaaggagatggcagaactgg 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 CCAAATTTCAGGAGCTGCGGTACAGTGTAGCCTTGGTCCTTAAGGAGATGGCAGAACTGG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 AGAAGAAGTGTGAGCGCAAACTGCAGGACTGACTGAACCCTGGTACTGTGGGTGCTGAAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 42; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.8%; Score 382.8; DB 42; 99.5%; Pred. No. 2.5e-97; iive 0; Mismatches 2;
/strain="Sprague-Dawley"
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/clone="UT-R-C2p-nz-d-10-0-UI"
/clone_lib="UT-R-C2p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1075 gcaactattaaaaaaaaaaaaa 1100
                                                                                                        /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.5
Matches 384, Conservative
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Best Local 8
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DEFINITION
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ORIGIN

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Gaps

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ACCESSION VERSION

RESULT AI048873

BASE COUNT 95 a ORIGIN	Query Match Best Local Similarity Matches 394; Conserv	Oy 77 atgcaactgtggtt 	Qy 137 tgctttgggggctg Db 76 rGcGrrGGGGGCrG	136 CAGITITCITG 257 Cttagacaga 196 CTTAGACAGG 317 agactgcaga 317 agactgcaga 377 ggccgtcctg	RESULT 8 A1154070 LOCUS A1154070 LOCUS A1154070 DEFINITION Ud76a06.rl Schools A1154070 VERSION A1154070 KEYMORDS EST. SOURCE ORGANISM WUS MUSCULUS EUTHORIS: ROCKATORIS AUTHORS GEATSOCKE: MAINER A1154070 REFERENCE 1 (bases 1) AUTHORS GEALSIAS, KI SCHOOLSTON	TITLE The WashD'-HH JOURNAL Unpublished COMMENT ON Jan 14, 12 CONTACT: MASHU-HHMI M WASHU-HHMI M WASHU-HHMI M WASHU-HMI SARWA 346 FRANK 314 286 FRANK 31
Oy 311 tgggaaagactgcagagaagctgtggagcaacttggtgccagcgccaacctgtcagaaga 370 	Oy 371 gegtetggcegtectgctgcgggcacacacactgctccagcaggctctccggctgcc 430	Qy 431 ccctgctagtctaaagccagatgccttccaggaagagctccaggaacttggcattcctca 490 	Oy 491 ggatctaattggagatttg 509 1	AA032667 AA032667 AA032667 AA032667 AA032667 AA032667 ACCESSION AA032667 AA032667.1 G1:1505234 EST CLONA AA032667.1 G1:1505234 KEYWORDS SOURCE ORGANISM AA032667.1 G1:1505234 AA032667.1 G1:1505234 KEYWORDS SOURCE ORGANISM AA032667.1 G1:1505234 AA032667.1 G1:1505234 KEYWORDS SOURCE ORGANISM AA032667.1 G1:1505234 AA03267.1 G1:1505234 AA03267.1 AA03267 AA03267.1 AA03267 AA03267.1 AA03267 AA03267.1 AA03267 AA04267 AA03267 AA04267 AA04267 AA04267 AA04267 AA04267 AA04267 AA04267	On Nov 29, Contact: Mash-HMM Washl-HMM Washlngton 4444 Fores Tel: 314 2 Fax: 314 2 Emal: mou This clone IMAGE Cons MGI:279021 Seq primer High quali	/issue_type="embryo" /fissue_type="million" /dev_stage="13.5-14.5dpc total fetus" /dev_stage="13.5-14.5dpc total fetus" /dev_stage="13.5-14.5dpc total fetus" /dev_stage="13.5-14.5dpc embryo" /det="vector: parmacla" is strand cDNA was primed with a Not I - 0.11go(dfl) primer [5'

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1111er, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., eg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eest@watson.wustl.edu
is available royalty-free through LLNL ; contact the
rtium (info@image.llnl.gov) for further information.
                                                                                                                                            taggacettetetteggactggteaagaaacgggaagaaaggatgte 136
                                                                                                                                                                                                                  gcagctccatacttgcaccatccgctgacagtcacagtggccgggt 196
                                                                                                                                                                                                                                                                                       teceagecetetecagaagtgaeggeegtggeteagetettgaagga 256
                                                                                                                                                                                                                                                                                                                                                             accttcagaaagttgttgaaacttgtagtcggggccctgcatgggaa 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gctgtggagcaacttggtgccagcgccaacctgtcagaagagcgtct 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                     Soares_mammary_gland_NMLMG Mus musculus cDNA clone 154 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMI Mouse EST Project 1 (1996)
1998 this sequence version replaced gi:1797639. Inra M/Mouse EST Project University School of MedicineP University School of MedicineP Parkway, Box 8501, St. Louis, MO 63108
                                                                                                            ö
                                                                   Score 373; DB 27; Length 444; Pred. No. 1.5e-94; 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -28m13 rev2 ET from Amersham
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 88
   р
 128
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                                                                   33.9%;
91.8%;
cvative
o <del>=</del>
133
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/strain="Status naveytes"
/strain="Status naveytes"
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/clone_lib="UI-R-BJ0p"
/dev_stage="adult"
/dev_stage=
                                                                                                                                                                                       Factorial to the vene biscovery and mapping University of Iowa 451 Eckstein Medical Research Building lowa City, IA 52242, USA 7e1: 319 335 9250

Tal: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligouclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized atrium at 15 doc library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 34-146, >PBIDD#SINE/Alu Seq primer: M13 Forward
facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     997 gtctgaggctggagaatgggaagtgtaagctgggcctggctttcatagtgaggctcagtg 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 TTGTTTTATGAGTCAACAGCTGGCAGGTGGCACAGTTTATAATCTCAGCCCTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              937 tttgttttatgagtcaacagctgggcagggtggcacagtttataatctcagcccttggaa
                                                                                                                gi:3137829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
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                                                                                     97044477
On May 18, 1998 this sequence version replaced
Contact: Scares, MB
Program for Rat Gene Discovery and Mapping
Normalization and subtraction: two approaches discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 334.4; DB 81;
Pred. No. 1e-83;
0; Mismatches 6; Ii

    .345
    /organism="Rattus norvegicus"

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TAG_TISSUM=atrium at 15 dpc
                                                   Genome_Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_SEQ=GAAGC
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Best Local Similarity 98.3%;
Matches 338; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 c
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ORIGIN
                                                                                        MEDLINE
COMMENT
                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
      TITLE
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                                                                                                                                                                                                /sex="female Golds.mammary gland"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/tasue_type="mammary gland"
/tasue_type="mammary gland"
/fasue_type="mammary gland"
/note="Vector: pT713D-pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT713 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
96 a 131 c 134 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cagiticcigggiticccagcccictccagaagigacggccgiggcicagcictigaagga 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 AGACTGCAGAGAGGCCGTGCACCATGGTG-CAGCGCCAACCTGTCAGAGGAGCGTCT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atgcaactgtggttaggaccttcttcggactggtcaagaaacgggaagaaaggatgtc 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgctttggggggctgcagctccatacttgcaccatcccgctgacagtcacagtggccgggt 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 GGCGTCCTGCTGGCGGGCACACACACTCCTGCTCCAGCA-GCTCTCCGGCTGCCCCTGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 345)
Bonaldo,M.F., Lennon, G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGTTGGGGGCTGCGGCTCCATACTTACACCATCCAACTGACAGTCACAGGGGGGGCGGGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggccgtcctgctggctggcgggcacacacaccctgctccagcaggctctccggctgcccctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                1. 454
/organism="Mus musculus"
/obxref="taxon:10090"
/clone="IMAGE:1476754"
/clone_lib="Soares mammary_gland_NMLMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 362; DB 42;
Pred. No. 1.9e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 aattggagatttggccagtttggcatttgggagt 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 GATTGGAGATCTGGCCAGTTTGCGATTTGGGAGT 454
      High quality sequence stop: 452.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW434638.1 GI:6965945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%;
ilarity 91.6%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW434638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416;
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Best Local S
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AW434638/c
LOCUS
DEFINITION
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1 (bases 1 to 540)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Shaon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Bullding (1998)

1 Unpublished (1998)

2 Other_GSSs: CIT-HSP-2338P5.TF

2 Ontart: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Sep primer: M13 Reverse
Class: BAC ends.
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105 GGCTGAGGCTGGAGAATGGGAAGTGTAAGCTGGGCCTGGCTTTCATAGTGAGGCTCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 teccag----ceetetecagaagtgaeggeegtggeteagetettgaaggaettagaeag
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                         Score 327.4; DB 94;
Pred. No. 1.2e-81;
0; Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Sperm"
/note="Vector: pBeloBAC11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2338P5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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AQ055548.1 GI:3352154
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ilarity 77.4%;
Conservative
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Best Local Simi
Matches 411;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Butherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 394)

I (bases I to 394)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelaing, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                    gotggogggaacacacacctgotccagcaggetotccggotgccccctgctagtotaaa 445
                       240 GCCTGACACTTCAGGGACCAGCTCCAGGAGCTCTGCATCCCCCAAGACCTGGTCGGGGA 181
                                                                                                                                                                          506 tttggccagtttgggcatttggggagtcaacgccctcttctgactctgtagcccaacagca 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m138h02.rl Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE:514323 5', mRNA sequence.
                                                                                                                                                                                                         gccagatgccttccaggaagagctccaggaacttggcattcctcaggatctaattggaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1966)
On Jan 25, 1995 this sequence version replaced gi:637728.
Contact: Marran MyMouse EST project
WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:514323"
/clone_lib="Stratagene mouse testis (#937308)"
                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 392.
Location/Qualifiers
1.394
/organism="Mus musculus"
/strain="Inbred CD-1"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse EST Project
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Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst (The ERATO/Doi Project at Wayne State University) Unpublished (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 569)
Ko,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
Grahovac,M.J., Mason,S., Lim,M.K., Paonessa,P.D., Sauls,A.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gatgagcccaactccattgaggtcctgcatgtgagaacgtattttaagtgaaaagacagc 923
||||||
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                                                                                                                                                                                                                                                                                                                                                                                              agggatectegeteaegtgtettaetteeggtggegggtggaegtggeeateteaa 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C77953 S69 bp mRNA EST 25-JUN-1996
C77953 Mouse 3.5-dpc blastocyst CDNA Mus musculus CDNA clone
                                                                                                                                                                                                                                                                                                                    505 atttggccagtttggcatttgggagtcaacgcctttttcgactctgtagcccaacagc
                                                                                                                                                                                                                                                                                                                                               1 ATCTGGCCAGTTTGGCATTTGGGAGTCAACGCCCTCTTCTCGACTCTGTAGCCCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 researtitieserritariariaransiares 145
                                                                                                                                                                                                                                                        DB 27; Length 446;
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                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                        Score 302.4; DB 27;
Pred. No. 1.2e-74;
0; Mismatches 46;
                                                                                                                                                                                               103
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/lab_host="DH10B"
                                                                                                                                                                                                                                                           27.5%;
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Best Local Similarity 84.3
Matches 398; Conservative
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1 (bases 1 to 446)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mousest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                        W83837 446 bp mRNA EST 12-SEP-1996 mf26c06.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:406186 5', mRNA sequence. W83837 GI:1540621
                                                                           256
                                                                                                                                                                                                                    tgetttgggggctgcagctccatacttgcaccatcccgctgacagtcacagtggccgggt 196
                                                                                                                                                         106 TGCGTTGGGGCTGCGGCTCCATACTTACACCATCCAACTGACAGTCACAGCGGCCGGGT 165
                                                   Gaps
                                                                                                                                                                                                      cagtttcctgggttcccagccctctccagaagtgacggccgtggctcagctcttgaagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Unpublished (1996)
Con Sep 12, 1996 this sequence version replaced gi:1394997.
Contact: Marra M.Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
H444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                   ö
                   Length 394;
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/dev_stage="13.5-14.5dpc total fetus"
                    DB 28;
                      Score 307.4; DB 28;
Pred. No. 4.4e-76;
0; Mismatches 26;
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:406186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="unknown"
                    Query Match 27.9%;
Best Local Similarity 92.6%;
Matches 323; Conservative
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Matches 312; Conserv
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                                                                                                                                                                                                                                                    460 aggaagagetecaggaaetteggeatteete-aggatetaattggagatttggeeagtt 517
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On Apr 18, 1995 this sequence version replaced gi:775302.
Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71,
Email: hd@bioa.jst.go.jp.
                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                              DB 36; Length 569;
                                                                                                                                    blastocyst cDNA'
                                                                                                                                                                      others
                                                                                                                                                                                                                                   46; Indels
                                                                                                                                                                                                            Score 296.6; DB 3
Pred. No. 5.6e-73;
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/dev_stage="3.5-dpc"
a 169 c 131 g 134 t
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Best Local Similarity 80.6%;
Matches 510; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eukarla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 374)

S Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubque,T., Gelsellenberg,K., Kleptoe,M., Tan,F., Underwood,K., Moore,B., Waterston,R.

Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and The WashU-HHMI Mouse EST Project

The WashU-HHMI Mouse EST Project
On Sep 12, 1996 this sequence version replaced gi:1394992.

All Oppublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1394992.

Asabington University School of Medicinep Washington University School of Medicinep Washington University School of Medicinep Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (imfo@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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/clone=1lb="Soares_mammary_gland_NDAMG"
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High quality sequence stop: 348.
Location/Qualifiers
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1larity 92.3%; Pred. No. 5.5e-73;
Conservative 0; Mismatches 26
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    .374
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Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst
(The EMATO/Doi Project at Wayne State University)
Unpublished (1997)
On Dec 3, 1996 this sequence version replaced gi:1119170.
Contact: Hirofumi Doi
Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bloa.jst.go.jp.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 574)
Ko,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T., Grahovac,M.J., Mason,S., Lim,M.K., Paonessa,P.D., Sauls,A.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgtcttacttccggtggcgggtggacgtggcatctcaaccagcgctcaqtcccgctcc 645
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C78711 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone
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3 a 170 c 136 g 133 t 2 others
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C78711.1 GI:2519041
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Search completed: May 14, 2000, 23:17:58 Job time: 16358 sec

Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SUMMARIES

							FEATURES	sonice																		DASE COUNT	ONTOIN		Query Matc	Best Local	Matches	00 627 00	3	Dp 545 CC		0y 687 tg		T 485 TC	Oy 747 tg	DD 425 TG	00 807	ò
Description	AA780068 zj24h04.s	AW005581 wz87h11.x		AW025527 wu97d10.x	AQ798652 HS_2238_B	MAG 2417 7 405 401 51	AA836105 od15001 s	AI276262 0155f06 x	AI240879 G194E02.x	AI076231 0y65c09.x	AW261921 xp87f11.x	AI189612 qd32g06.x	AA857959 oe33g04.s	AA464962 ZX80106.s	ALZUULZ9 GI9UNUS.X R20463 ****33400 ~1	W86177 zh59011 e1	A1274473 gv61c09.x	AI004350 019506.x	AA994284 ou50a05.s	N49076 yy79b07.s1	AI336855 qx86g08.x	AA737662 nw59d12.s	AI248784 qh67b01.x	AND TOTAL TELEVISION	AMOLIUSE OBESEUS.S	W92692 zh79d09.s1	AA029291 zk10b06.s	A1470273 tj18g08.x	N74187 za76h04.sl		AA780382 aa67502 s				AWZ4836/ Z8Z1036.3	M920/2 ZD/9009.Tl			mi49al			
ID 8	18 AA780068										9 AW261921					_	-	-	-		3 A1336855						-				3 AA780382			A1400947	-					AT.TGNAENTS		
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OTHER WILL			Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997) On Jan 9, 1998 this sequence version replaced gi:936306.
	RESULT 1 AA780068/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	OKGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT

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1. 548

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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 507.
Location/Qualifiers
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Pred. No. 3.5e-125;
0; Mismatches 3; Indels 0;
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Eukaryotta; Matazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 540)

RS Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

AL Upublished (1998)

Other_GSS: CIT-HSP-2338P5.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

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Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.
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                                                                                                                                                                                                                               AQ055548 540 bp DNA GSS 30-JUL-1998
CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5,
genomic survey sequence.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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tctccaccagtgccctggctccctgcagccgagcgtcctgatgcagctgaagcttt
                                                                                                                                                            cagatgggtcagcataccgcattgaggtccccacaggccaagttccaggagctgcggtaca
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1. .540
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="238895"
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINI at:
www-bio.llnl.gov/bbrp/image/image.html
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IMAGE:2565861 3',
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E 1 (bases 1 to 520)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

L Obsorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index

Unpublished (1998)

On Jun 5, 1998 this sequence version replaced gi:3187080.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
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wz87h11.x1 NCI_CGAP_BIn25 Homo sapiens cDNA clone
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Pred. No. 1.1e-117;
0; Mismatches 2;
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/db_xref="taxon:9606"
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High quality sequence stop: 452.
Location/Qualifiers
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AW005581
AW005581.1 GI:5854359
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Best Local Similarity 99.6
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www-bio.llnl.gov/bbrp/1mage/image.html
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1 (bases I to $25)

NCI/NINDS-GGAP http://www.ncbi.nlm.nh.gov/nclcgap.
National Cancer Institute / National Institute of Neurologica Disorders and Stroke, Brain Tumor Genome Anatomy Project (GGAP/BTGAP), Tumor Gene Index
Unpublished (1993)

On Dec. 20, 1995 this sequence version replaced gi:1131323.
Contact: Robert Strausberg, Ph.D.
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                                                4
                      Length 540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausbergenih.gov
Hissue Procurement: David N. Louis, M.D., Myrna R.
                                               Indels
                      Score 504.4; DB 94
Pred. No. 4.6e-116;
0; Mismatches 6;
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A1871472
A1871472.1 GI:5545521
                    Query Match 37.2%;
Best Local Similarity 98.1%;
Matches 522; Conservative
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Email: Robert etre
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                                                                                                                                                                                                                                                                                                  Score 503; DB 61; Length 525;
Pred. No. 1e-115;
0; Mismatches 5; Indels
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High quality sequence stop: 453.
Location/Qualifiers
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Best Local Similarity 98.9%;
Matches 517; Conservative 0
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                          AQ798652 501 bp DNA GSS 09-AUG-1999 HS_2238_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=5 Row=P, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (206) 616-3618
Fax: (206) 616-3617
Fax: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

1 163 c 139 g 92 t 2 others
        1013 acctgagatggtgccaaagtgcagctgactcttcccacgacagccttggccttcccatca 1072
                                           167 ACCTGAGATGGTGCCAAAGTGCAGCTGACTCTTCCCACGACAGCCCTGCCCTTCCCATGA 108
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/clone_limp="CIT Approved Human Genomic Sperm Library /sex="male"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) . 99380589
                                                                                                                       ggcaggctcttcagtgagtgtttgaacgtaattatgtagttttctgtttaattgaaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 10, 1998 this sequence version replaced gi:3553660. Contact: Mahairas GG, Wallace JC, Hood L L Handupput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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                                                                                                                                                                                                                             33.0%; Score 447; DB 90;
94.4%; Pred. No. 1.1e-101;
live 0; Mismatches 27;
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                                                                                                                                                                                                           Tumor Gene Index

Inpublished (1997)

On Jun 5, 1998 this sequence version replaced gi:3187612.

Contact: Robert Strausberg, Ph.D.

Tal: (301) 496-1550

Email: Robert-Strausberg@uih.gov.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CLOR Gistribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.html
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112 t
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 527)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:2527987"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH108"
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High quality sequence stop: 444.
Location/Qualifiers
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nes 517; Conservative
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Homo saplens
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
1 (bases 1 to 37)
1 (bases 2 to 37)
1 (bases 2 to 37)
1 (bases 3 to 10 to 
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1172 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 348.
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                                                                                                                       tttgtggtcagcagcctgcagggggaggactgccgagacggtgtgcagcgtcttgggggtc
                                                           381 TITIGIGGICAGCAGCTIGCAGGGGAAGAACTGCCGAGAGICTGIGCAGIGICITIGGGGIC
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone="IMAGE:470099"
/clone_lib="Soares_pregnant_uterus_NbHPU"
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/organism="Homo sapiens"
/db_xref="GDB:3756101"
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AA029831.1 GI:1496076
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                                                                                                                                                                                                                                                        agcaggcctccgtctgcccccaccagcctgaagcctgacaccttcagggaccagctcc
                                                                                                                                                                                                                                                                                                                                            AGCAGGCCCTCCGTCTGCCCCCCCAGCCTGAAGCCTGACACCTTCAGGGACCAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hawkins, M.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Pinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 491)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawki
                                                                                                                            Score 441.2; DB 27; Length
Pred. No. 3.1e-100;
0; Mismatches 11; Indels
                                                                                                                             32.6%;
llarity 96.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:1422688
                                                                                                                                       Similarity
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W93417.1
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Best Local Simil
Matches 524; C
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W93417/c
LOCUS
DEFINITION
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                                                                                        COUNT
                                                                                                                                                                   335
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AUTHORS
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AA836105/c
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AUTHORS
TITLE
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/db_xref="GDB:1273761"
/db_xref="GDB:1273761"
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/clone="InBage:387217"
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/clone="InBage:387217"
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/dev_stage="19 weeks"
/dev_brost="Deverty"
/dev_stage="19 weeks"
/dev_stage="19 weekss"
/dev_stage="10 weekss
                                                                                                                   Unpublished (1995)
On Sep 21, 1992 this sequence version replaced gi:279425.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 375.
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          Marra, M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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32.5%; Score 440.8; DB 26
Best Local Similarity 97.3%; Pred. No. 3.8e-100;
Matches 468; Conservative 0; Mismatches 10;
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Sequencing Center
information can be
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Dipublished (1997)
On May 5, 1995 this sequence version replaced gi:797662.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenin.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP chone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                   AA836105 447 bp mRNA EST 25-MAR-1998
odi5c01:s1 NCI_CGAp_GCB1 Homo sapiens cDNA clone IMAGE:1368000,
124 GCCCTGCCCTTCCCATGAGGCAGGCTCTTCAGTGAGTGTTTGAACGTAATTATGTAGTTT 65
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Pred. No. 9.3e-97;
); Mismatches 3; 1
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High quality sequence stop: 441.
Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                       AA836105.1 GI:2910424
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Best Local Similarity 99.3%;
Matches 429; Conservative (
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AA836105
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AL276262 437 bp mRNA EST 29-JAN-1999
4155f06.x1 Scares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877219
3', mRNA sequence.
AL276262
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/tissue_lip="Pooled human melanocyte, fetal heart, and pregnant uterus"
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 437)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2282464.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nth.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image:llnl.gov) for further information.
Insert Length: (20) 5td Error: 0.00
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               tgaggtccccacagccaagttccaggagctgcggtacagcgtggccctggtcctaaagga
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High quality sequence stop: 436.
Location/Qualifiers
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NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-348479."
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                                                                                                                                                                                           44; Length 437;
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Email: Robert_Strausberg@nlh.gov
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/db_xref="taxon:9606"
/clone="Inhest:1867130"
/clone=lib="NoLI-GAP_Kid3"
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oy65c09.x1 NCI_CGAP_CLL1 Homo sapiens CDNA clone IMAGE:1670704.3',
  Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.7e-93;
0; Mismatches 2; Indels 0;
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                                                                                                  Std Error:
                                                                                                                         Seq primer: -40UP from Gibco
High quality sequence stop: 404.
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99.5%;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
On Jan 19, 1998 this sequence version replaced gi:2152808.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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/clone_lib="NCI_CGAP_CLI"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 406.8; DB 42;
Pred. No. 1.2e-91;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                           Insert Length: 1034 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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.larity 99.5%;
.conservative (
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RESULT 14
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Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 411)

Notional Cancer to 411)

Notional Cancer Institute / National Institute of Neurological Stroke, Brain Tumor Genome Anatomy Project (CGAP/PETGAP); Tumor Gene Index

(CGAP/PETGAP); Tumor Gene Index

(CGAP/PETGAP); Tumor Gene Index

(CONTACT: Robert Strausberg, Ph.D.

On Jun 5, 1998 this sequence version replaced gi:3189186.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg on Ph.D.

Contact: Robert Strausberg on Ph.D.

Contact: Robert Strausberg on Ph.D.

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life

Technologies, Inc. CDNA Library Preparation: Life

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LIM at:

Www-bio.llnl.gov/bbrp/image/image.html
                                     AW261921 411 bp mRNA EST 28-DEC-1999
XPM 711.x1 NCI_CGAP_Brn53 Homo sapiens CDNA clone IMAGE:2747373 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:2747373"
/clone="IMAGE:2747373"
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/lab_host="DH10B"
/note="Yorgan: brain; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies."
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Seq primer: -400P from Gibco
High quality sequence stop: 396.
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                                                                                                           AW261921.1 GI:6638737
                                                                         mRNA sequence.
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Euthorias papiens
Euthorias, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Euthoria; Primates; Catarrhini; Hominidae; Homo.
Euthoria; Primates; Catarrhini; Hominidae; Homo.
Euthoria; Primates; Catarrhini; Hominidae; Homo.

NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
On May 9, 1995 this sequence version replaced gi:803101.
Contact: Robert Strausberg, Ph.D.
Trai: (301) 496-1550
Contact: Robert Strausberg, Ph.D.
Trai: (301) 496-1550
Email: Robert_Strausberg@ih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1048 std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 391.

This Contact of the state of the sequence stop: 391.
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                                                                                                                                                                                                                                                                          AI189612 418 bp mRNA EST 28-OCT-1998 qd32g06.xl Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens CDNA clone IMAGE:1725466 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9w"
/dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
1067 ccatcaggcaggctcttcagtgagtgtttgaacgtaattatgtagttttctgtttaattg 1126
                       767 gggtggatgtagcaatctccaccagtgcctggtcgctccctgcagccgagcgtcctg 826
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                                                                                          Query Match 29.9%; Score 405.8; DB 43; Length Best Local Similarity 99.5%; Pred. No. 2.1e-91; Matches 407; Conservative 0; Mismatches 2; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:1725466"
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                               AMBS7959 410 bp mRNA EST 25-MAR-1998 0833904.s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1410390 3', AA857959
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2284841.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
 9t9agcgcagactgcaggactgaccctcacttgaccagtcccattcagatccggcttgg 1006
                                                          ccatcaggcaggctcttcagtgagtgtttgaacgtaattatgtagttttctgtttaattg 1126
                          238 GTGAGGGGAGACTGCAGGACTGACCTTGACCAGTCCCATTCAGATCCGGCTTGG
                                                                                                                                  DB 39; Length 410;
                                                                                                                                                                             1127 aaaaagagagctatgcctttttttttggaagtaaagcagctaaaa 1175
                                                                                                                                                                                              Insert Length: 1238 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 401. Location/Qualifiers
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Best Local Similarity 99.5
Matches 398; Conservative
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110 AGCTCTTCAGTGAGTGTTTGAACGTAATTATGTAGTTTTCTGTTTAATTGAAAAAGAGA
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Sequence 5, Sequence 5, Sequence 5, Sequence 4, Sequence 11, Sequence 11, Sequence 28, Sequence 2, Sequence 2, Sequence 17, Sequence 17,
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    Sequence 3
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Sequence 5
Sequence 5
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTR: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: INDAPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,463
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
PCT-US95-06743-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER, 30472/114 IMMU TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY-AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                   ; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 899149
INFORMATION FOR SEQ ID NO: #14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : (703)836-9300
(703)683-4109
  6306
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1294
3357
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                     May 14, 2000, 22:50:12 ; Search time 76.12 Seconds (without alignments) 1834.863 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5E_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
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7: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-724-394A-21
US-08-724-394A-21
US-08-550-75-1
US-08-550-75-1
US-08-422-699A-10
US-08-422-706B-10
US-08-422-706B-10
US-08-414-095-7
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US-08-487-799-1

US-08-920-812-13

US-08-921-177-13

US-08-921-177-13

US-08-921-177-13
                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
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US-08-486-756A-44
US-08-485-862B-44
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                                                                                                                                                                                                                                              226296 seqs, 63486255 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                nucleic search, using sw model
                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                US-09-223-796-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 1000000
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2908
9515
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246240
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126240
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Match Length
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3323
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1334
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                                                                                                                                              Title:
Parfect score:
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        KORAN
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        KORAN
        46444

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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE:
US-08-627-254C-26
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
JS-08-627-254C-26
                                                                   US-08-629-643A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CENGTH:
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                                                                                                     867 gagcccaactccattgaggtcctgcatgtgagaacgtatttaagtgaaaagacagcggg 926
                                                                                                                                                                                                                                                                          actttcaggtttttgttttatgagtcaacagctgggcagggtggcacagtttataatctca 986
                                                                   747 ttggtccttaaggagatggcagaactggagaagaagtgtgagcgcaaactgcaggactga 806
                                                                                                                                      807 ctgaaccctggtactgtgggtgctgaagctggtaccagaacacagcccccactggtgat 866
                                                                                                                                                                                                                                                                                                                                                                                                               Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUNKESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A. STREEI: P. O. Box 2938
CITY: Minneapolis
STATE: MN
Query Match 4.1%; Score 45.6; DB 1; Length 7
Best Local Similarity 1.7%; Pred. No. 0.00087;
Matches 6; Conservative 207; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lee, J. L.
APPLICANT: Lee, N. A.
TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
APPLICATION NUMBER: US/08/629,643A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLOSSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/629,643
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: VIKSNIA: Ann S
REGISTRATION NUMBER: 37,748
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08629643A Patent No. 6025539 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-359-3263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-629-643A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                              921 agcgggactttcaggttttgttttatgagtcaacagctgggcagggtggcacagtttata 980
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                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.4%; Score 37.2; DB 3; Length 2757; Best Local Similarity 54.5%; Pred. No. 0.17; Hatches 97; Conservative 0; Mismatches 78; Indels 13.
                                                                                                                                                                              Length 6727,
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRETT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,254C
                                                                                                                                                                                                                                     86;
NAME/KEX: mat_peptide
LOCATION: 650...377
O'THER INFORMATION: Join 650..730, 1560..1592,
OTHER INFORMATION: 3468..3596, 3676..3771
                                                                                                                                                                              Ouery Match

3.4%; Score 37.4; DB 5;
Best Local Similarity 50.9%; Pred. No. 0.22;
Matches 89; Conservative 0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Calfee, Halter & Griwold LLP STREET: 800 Superior Avenue CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/08627254C
Patent No. 585929
GENERAL INFORMATION:
APPLICANT: Kniss, Douglas A.
TITLE OF INVENTION: Eicosanoid Formation
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: GOITICK, MATY E
REFERENCE/DOCKET NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 18525/00107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEO ID NO: \\(\bar{1}\)225
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA to mRNA
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STRANDEDNESS: double
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tataateteageeettggaagtetgaggetggagaatgggaagtgtaagetgggeetgge 1036
                                         2652 CTACAGAGTGAGTTCCAGGATAGCCAGGGCTACACAGAGAAACCCTGTCTTGAAAAACAA 2593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IELOPPY GLEAK
COMPUTER: DEC COMPAÑADLE
OPERATING SYSTEM: PC-DÓS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,628
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.35;
0; Mismatches
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/380,403
FILING DATE: 30-JAN-1995
APPLICATION UNDRER: US 08/325,909
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                           Sequence 3, Application US/08895628
Patent No. 5998585
GENERAL INPORMATION:
APPLICANT: MINATO, Nagahiro
APPLICANT: HATORI, Masakazu
APPLICANT: HIROSHI, Kubota
APPLICANT: MASATSUGU, Maeda
: TITLE OF INVENTION: SPA-1 PROTEIN
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 6-279712
FILING DATE: 20-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY, AGGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25,258
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5687 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.3%;
ilarity 56.1%;
Conservative
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(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSE: Foley & I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 69; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
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US-08-895-628-3
                                                                                                             111
2592 AAA 2590
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US-08-895-628-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  977 tataateteagecettggaagtetgaggetggagaatgggaagtgtaagetgggeetgge 1036
                                       985 cagcccttggaagtctgaggc---tggagaatggaaagtgtaagctgggcctggcttca 1041
2170 CAGCACTIGGAAGGCAGAGGCAGIIGGAICTCIGGGAGIIIGAGGCCAGIIIGGCCIAIA 2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: MINATO, Nagahiro
APPLICANT: HATTORI, Masakazu
APPLICANT: HAGOSHI, Kubota
APPLICANT: HAGOSHI, Kubota
APPLICANT: MASATSUGU, Maeda
APPLICANT: MSATSUGU, Maeda
APPLICANT: SPA-1 PROTEIN AND GENE CODING THEREFOR NUMBER OF SEQUENCES: 7
CORRESPONDENCE. ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36.6; DI
Pred. No. 0.35,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 53466/128/AAOK
TELECOMMUTICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,909
FILING DATE: 19-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-279712
FILING DATE: 20-CCT-1994
PRIOR APPLICATION NUMBER: UP 6-139513
APPLICATION NUMBER: 30-MAX-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/380,403A
FILING DATE: 30-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITX:
CITX:
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Repopt disk
COUNTRY: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                     Sequence 3, Application US/08380403A
Patent No. 5831024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.3%;
Best Local Similarity 56.1%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
ERNGTH: 5687 base palrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 A
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MINATO,
                                                                                                                                                                                                                                      SULT 4
-08-380-403A-3/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-380-403A-3
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Pred. No. 0.51;
0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ohno, Tsuneya
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PELLCATION UNDER: US/08/920,812
FILING DATE: 29-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: 6300 CITY: Chicago STATE: 1111nois COUNTRY: United States of America 21P: 60606-6402 CITY: TRABABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606-6402
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       RESULT 6
US-08-487-799-1
Squence 1, Application US/08487799C
; Patent No. 6010908
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Patent No. 5763188
GENERAL INFORMATION:
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Best Local Similarity 71.2%;
Matches 47; Conservative
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 ataaaa 191
                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: human
US-08-487-799-1
                                                                                          2592 AAA 2590
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US-08-920-812-13/c
                                                             1097 aaa 1099
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LENGTH: 2908
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1222 GACCTCGGTGGAGCCGGTGAACACCAGTGCGTCCGGGTGCAAGCCGAGGCCTT 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Matsuhisa, Akio
APPLICANT: Matsuhisa, Akio
APPLICANT: Matsuhisa, Akio
APPLICANT: Ghno, Tsuneya
APPLICANT: Geda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREE: 1000 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STRTE: 111nois
COUWTRY: United States of America
ZIP: 60606-6402
COWPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EDOPPY disk
COMPUTER: EDOPPY disk
COMPUTER: EDOPPY disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
ATORNEZ/AGENT: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
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Best Local Similarity 56.5%; Pred. No. 1.3;
Matches 65; Conservative 0; Mismatches 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-WAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: RIL-Lauters, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 1936/32420
TELECOMMUNICATION INFORMATION:
TELECHONE: 312/474-6300
TELERAX: 312/474-6300
TELERAX: 25-386
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERNCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       טראסאונט Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
US-08-920-812-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08920827; Patent No. 5770375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: GORIGINAL SOURCE: ORGANISM: Pseu
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US-08-920-827-13/c
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1222 GACCICGGIGGAGCCGGIGAACACCAGIGCGICCACCICCGGGIGCAAGCCGAGGGCCIT 1163
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                                                                                                                                                                                                      Gaps
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APPLICANT: Matsuhisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
                                                                                                                                                     Score 35; DB 2; Length 9515;
Pred. No. 1.3;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.2%; Score 35; DB 2;
Best Local Similarity 56.5%; Pred. No. 1.3;
Matches 65; Conservative 0; Mismatches 5:
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27-MAR-1995
                       ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
US-08-921-177-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANAMAISM: Pseudomonas aeruginosa STRAIN: Clinical Isolate P2-2 US-08-362-577C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 13, Application US/08362577C
; Patent No. 5807673
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ATTORNEY/AGENT INFORMATION:
NAME: RID-LAURES, LI-HBIEN
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 1903
TELECOMMUICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pairs
                                                                                                                                              Query Match 3.2%;
Best Local Similarity 56.5%;
Matches 65; Conservative
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MOLECULE TYPE: Genomic DNA
OPTGINAL SOURCE:
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                  ORIGINAL SOURCE
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-362-577C-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                          Length 9515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Marshail, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                    50; Indels
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STATE: Illing's

COUNTRY: United States of America

ZIP: 6060-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/921,177

FILING DATE: 29-AUG-1997

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                 Query Match
3.2%; Score 35; DB 2
Best Local Similarity 56.5%; Pred. No. 1.3;
Matches 65; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19036/32420
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            MOLECULE TYPE: Genomic DNA
CRIGINAL SOURCE:
ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
US-08-920-827-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08921177
Patent No. 5798211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 1903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6480
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear.
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9515 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ohno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Se
CITY: Chicago
STATE: Illinois
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Db 14797 CTTTGGGAGGCTGAGGAGGAGCGTTGAGCAAGACCAGCCTGGGCAACATAGTGAG 14738
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Pred. No. 2;
0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(7540..7650, 9814..9945, 10421..10519
11602..11787)
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,011
FILING DATE: 11-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                  ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ADDRESSEE: ROBERTS & CUSHMAN STREET: 130 Water Street
STREET: Boston
STATE: Massachusetts
                                                                       APPLICANT: ONDA, Haruo (1)
APPLICANT: KIMURA, Chiharu
APPLICANT: OHKUBO, Shoichi
IITLE OF INVENTION: NOVEL DNA AND USE THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 14737 ACCTGGCCACTAAAATAAAAATAAAAGAACAAT 14704
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,246
FILING DATE: 13-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,676
FILING DATE: 07-AUG-1991
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US-08-724-394A-20
; Sequence 20, Application US/08724394A,
Patent No. 5872237
; GENERAL INFORMATION:
Sequence 1, Application US/08076011 Patent No. 5521069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S
REGIESTRATION NUMBER: 34.35
REFERENCE/DOCKET NUMBER: 411:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2%;
Best Local Similarity 60.6%;
Matches 57; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERA: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER.EICS:
LENGTH: 17041 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                       02109
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US-08-076-011-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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       1222 GACCTCGGTGGAGCCGGTGAACACCAGTGCGTCCACCTCCGGGTGCAAGCCGAGGGCCTT 1163
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APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Watsuhisa, Akio
APPLICANT: Eda, Soji Hrotsugu
APPLICANT: Eda, Soji Frobe for Diagnosing Infectious Disease
ITITE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STRRET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6660-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 443-1997
                                                                                                                                                                                                                                                                                                                                                                                                     Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 9515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.2%; Score 35; DB 3
Best Local Similarity 56.5%; Pred. No. 1.3;
Matches 65; Conservative '0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: RID-Lautes, LI-Hsien
REGISTRATION NUMBER: 33.547
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa STRAIN: Clinical Isolate P2-2 US-08-920-828-13
                                                                                                                                                                                                                          Sequence 13, Application US/08920828
Patent No. 5853998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCULG TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 9515 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                RESULT 11
US-08-920-828-13/c
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US-08-076-011-1/c
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Gaps

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990 ettggaagtetgaggetggagaatgggaagtgtaagetgggeetggettteatagtgagg 1049
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Pred. No. 7;
0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Megabase Transcript Map: No. 58 TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                     CCOUNTRY: USA

ZUR: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PEACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLAN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: S36
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
RESISTRATION NUMBER: 35.136
REFERENCE/DOCKET NUMBER: 017957-000100
TELEPRONE: 415-576-0200
TELEPRONE: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
'FWARTH PATENTIN FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Sequences and Antibodies Thereto NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: TOWNSEND and TOWNSEND and CREW STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ): NAME/KEY: misc_feature

): LCOATION: 1..246240

): OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS: not relevant
not relevant
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Best Local Similarity 57.3%;
Matches 63; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-724-394A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.8; DB 3; Length 246
Pred. No. 7;
0; Mismatches 47; Indels
                                            APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Megabase Transcript Map:
                                                                                                                                                                                                                                            ADDRESSEE: TOWNSEND and TOWNSEND and CREW STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
| LOCATION: 1..246240
| OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-724-394A-21

Sequence 21, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lauer, Peter M.
Ruddy, David A.
Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246740 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.2%;
Best Local Similarity 57.3%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kronmal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: F
APPLICANT: K
APPLICANT: L
APPLICANT: R
APPLICANT: R
APPLICANT: T
APPLICANT: T
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LF

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COMPUTER RADALE FORM:
MEDIUM TYPE: TIOPPY disk
MEDIUM TYPE: TOPPY disk
MARE: PILLNG DATE: 01-07-196
MATCHERD TAPPICATION DATA: 39.4A

FILLNG DATE: 01-07-196
MATCHERD TYPE: MEDIUM TYPE TOPPY DATA: 35.136
MATCHERD TYPE: MEDIUM TYPE TOPPY TYPE: MEDIUM TYPE TOPPY TYPE: MEDIUM TYPE TOPPY TYPE: MEDIUM TYPE: MEDI
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Search completed: May 15, 2000, 01:50:08 Job time: 10796 sec

OM nucleic - nucleic search, using sw model

Run on:

May 14, 2000, 23:02:16 ; Search time 84.19 Seconds (without alignments) 3268.931 Million cell updates/sec

US-09-223-796-1 Title: Perfect score:

Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

311585 seqs, 125096042 residues

Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 08 Listing first 45 summaries

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	נו ו	C I	Proliferation-inhi	Viral infection ge	- au	Unique 2.9 kb geno	Mouse cell cycle r	Mouse 1-alpha-OHas		neutroph	r repression	AS-30D tumour Type	Mouse butyrophilin	DNA encoding a hum	Human secreted pro	hNBC3a coding segu						PACPAP38 DNA. PACA	Hereditary haemoch	Human U62317 gene		Human prothrombina	Mouse 1-alpha-OHas	Human myotonic dys	Mouse 1-alpha-OHAS	Ω	Rat acyl peptide h	Human kidney amino	Human brain Expres	Sequence encoding
SUMMARIES		ជា	V18890	V18891	T32035	V06127	T88014	Q75270	T65001	X23315	X20419	V33755	Q72975	T78598	V05159	x51728	X37460	X18193	X18192	T89399	T89396 ·	055145	021065	067057	V57903	X18941	V43607	V84139	X23318	Q48675	X23316	T89885	005243	X23517	Q61201	Q54841
		BB	1	-		ч	~1		7	-	Н	, -1	~	Н												Н	~ I	_	-	_	-	٦	Н	-	н	 1
		Match Length	1100	701	218	849	6727	2858	5687	4736	602	1371	2851	5150	14180	921	1089	2880	3912	2458	8353	9515	17041	_	237326	2560	1573	4630	1698	3323	4105	2344	13206	50000	392	9089
æ	Query	Match	100.0	13.6	3.8	3.6	3.4	3.3	3.3	ж Э, Э	3.3	3,3	т Э	э. Э	3.3	3.3	3.5	3.5	3.5	3.5	3.2	3.5	3.5	3.2	3.5	3.1	 	3.1	3.1	3.1	3.1	3.0	3.0	3.0	3.0	3.0
	,	Score	1100	149.2	41.4	39.8	37.4	36.6	36.6	36.4	36.2	36.2	36.2	36.2	36.2	35.8	35.4			35	35	m	4	4	4.	34.2		٠. ن	'n.	m.	m.		33	m	32.8	o,
	Result	No.	1	7	m	O 4	'n		c 2			c 10	H	12	c 13	14	15	16	17	18	19			c 22		24	52	97	17	28	53	30	31		33 0	34

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cDNA encoding LexA	MuTu putative onco	Process cognate of	Prostate-tumour de Human prostatic sp	Mus musculus EPCR Cellulose synthase	Human adult brain
T77783 T77782	T09187 X37545	T60587 X27277	X27262 T61701	V19608 Q53522	V73002
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6579	10897	1294	5668	3360	1908
0.0	9.0	0.0	0 0 0 0	9.9	2.9
32.8 32.8	32.8	32.6	32.6	32.4 32.4	32
35	37	39	41	44	45
	O	O		U	

ALIGNMENTS

V18890	RESULT 1
DY 18899 standard; CDNA; 1100 BP. We structured the standard additum regulated gene; HCaRG; rat parathyroid; RW extracellular calcium concentration; antibody; hypertension; ss; Wy bettension related calcium regulated gene; HCaRG; rat parathyroid; RW extracellular calcium concentration; antibody; hypertension; ss; Wy cancer; inflammatory disease; asthma. Sancer; inflammatory disease; asthma. Sancer; inflammatory disease; asthma. Sattacellular calcium concentration; antibody; hypertension; ss; PK w cancer; inflammatory disease; asthma. Sattacellular calcium concentration; antibody; hypertension; stroke; CARG; 131. 130. FY CARG; Inflammatory disease; asthma. Mo9148807-A2. Anote="EF-hand like motif" antibody antibody of the motif" antibody antibody of the motif" antibody antibody of the motif" antibody according to the motif antibody addition and the motif antibody addition and to detect, e.g. hypertension related calcium regulated gene (RCARG), which was isolated from the rat parathyroid. This nucleic acid sequence encodes the hypertension related calcium regulated gene (RCARG), which was isolated from the rat parathyroid. This nucleic acid sequence encodes the hypertension or equilated gene (RCARG), which was isolated from the rat parathyroid. This nucleic acid sequence encodes the hypertension or equilated gene (RCARG), which was isolated from the rat parathyroid cancer, and antibody adding the protein, can be used to detect or modulate concentration and encodes the protein, can be used to detect or modulate or inflammatory diseases, and asthma. Second inflammatory diseases, and asthma and antibody adding the protein. Ouery Match 1100, Conservative 0, Mismatches 0; Indels 0; Gaps Matches 1100; Conservative 0, Mismatches 0; Indels 0; Gaps	W18890 standard; cDNA; 1100 BP. V18890; W18890; W18840; W18890; W1890; W1990;
V18890 standard; CDNA; 1100 BP. V18890 standard; CDNA; 1100 BP. O9-UNN-1998 (first entry) Rat Hypertension related calcium regulated gene (HCaRG) cDNA. Hypertension related calcium regulated gene; HCaRG; rat parathy extracellular calcium concentration; antibody; hypertension; stepoprosis; heart failure; diabetes; stroke; cancer; inflammatory disease; asthma. Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Arage a My9749807-A2. 31-DEC-1997. 23-UNN-1997; CA0439. 21-JUN-1996; US-667495. (GOSSA, GOSSAA, E. F. Hamet P. Lewanczuk R. Tremblay J; Rember P. Lewanczuk R. Tremblay J; Respectable Calcium regulated gene - useful to develop products to treat or detect, e.g. hypertension, stroke, cancer, diabetes or asthma Claim Z; Pages 25-56; Agpp: English. Hypertension related calcium regulated from the rat parathy Its sexpression is regulated by extracellular calcium concentration with such colds against the protein, can be used to detect or modula claim 2; Pages 25-56; Agpp: English. This nucleic acid sequence encodes the hypertension, They can specifically be used to detect or treat, e.g. hypertension, hyperthyroidism, osteoporosis, heart failure, diabetes, stroke, inflammatory disease, and asthma sequence 1100 BP; 260 A; 279 C; 315 G; 106 C; Ratch Match Duery Match Duery Match Duery Match Sequence 1100 BP; Pred, No. 0, 0, 10, 10, 10, 10, 10, 10, 10, 10, 1	9890 V18890 standard; CDNA; 1100 BP. V18890; V18890 standard; CDNA; 1100 BP. V18890; Standard; CDNA; 1100 BP. V18890; Standard; CDNA; V18890; Standard; Standard; Status related calcium regulated gene; HCaRG; rat parathy) extracellular calcium concentration; antibody; hypertension; standard; osteoporosis; heart failure; diabetes; stroke; cancer; inflammatory disease; asthma. Nyperthyroidian; osteoporosis; heart failure; diabetes; stroke; status; Location/Qualifiers CDS (*tag- a
V18890 standard; CDNA; 1100 BP. V18890 V18890 V1890 standard; CDNA; 1100 BP. V1890; V1800; V1800; V1800; V1900; V1	V18890 standard; CDNA; 1100 BP. V18890; V18890; V18890; V18890; V18890; V18890; V18890; Nat Hypertension related calcium regulated gene; HCaRG; rat parathy extracellular calcium concentration; antibody; hypertension; ss, hypertension related calcium regulated gene; HCaRG; rat parathy extracellular calcium concentration; antibody; hypertension; ss, hypertyroidism; osteoporosis; heart failure; diabetes; stroke; ratus; Location/Qualifiers Rattus rattus. Key J131. 806 Artag= B MO9749807-A2 J17804 MO9749807-A2 J17804 MOS749807-A2 J17804 MOS749807-A2 J17804 MOS749807-A2 J17804 MOS749807-A2 J17804 MOS749807-A2 MOS7805 MOS7805 MOS7805 MOS7805 MOS7805 MOS7806 MOS
V18890 standard; CDNA; 1100 BP. V18890; V18890 standard; CDNA; 1100 BP. V18890; V1890; V190;	V18890 standard; CDNA; 1100 BP. V18890; V18890; V18890; V18890; V18890; V18890; Nat Hypertension related calcium regulated gene; HCaRG; rat parathy extracellular calcium concentration; antibody; hypertension; ss, hypertension related calcium regulated gene; HCaRG; rat parathy extracellular calcium concentration; antibody; hypertension; ss, hypertension related calcium regulated gene; inflammatory disease; asthma. Rattus rattus. Location/Qualifiers Rattus rattus. Location/Qualifiers Rey 131. 806 / Ftage
V18990 standard; cDNA; 1100 BP. V18990; V18990; V18990; V18990; V18990; V18990; Sat Hypertension related calcium regulated gene; Hyderfension; saturathy extracellular calcium concentration; antibody; hypertension; saturathy extracellular calcium concentration; antibody; hypertension; saturation; related calcium regulated gene; Hypertension; saturation; related calcium concentration; saturation; satu	V18890 standard; CDNA; 1100 BP. V18890; V18890 standard; CDNA; 1100 BP. V18890; V1890; V1890; V1890; V1890; V1890; V1890; Satur-1998 (first entry) Rat Hypertension related calcium regulated gene; HCaRG; rat parathy extracellular calcium concentration; antibody; hypertension; ss, hyperthyroidism; osteoporosis; heart failure; diabetes; stroke; cancer; inflammatory disease; asthma. Rattus rattus. Location/Qualifiers Artag= a /Product= "Hypertension related calcium regulate insc_1997; CA0439. Z1-UN-1997; CA0499. Z1-UN-1997; CA0499. Z1-UN-1997; CA0499. Z1-UN-1997; C
V18990 standard; cDNA; 1100 BP. V18990; V18990; V18990; V18990; V18990; V18990; Sat Hypertension related calcium regulated gene; HcZeKG; rat parathy extracellular calcium concentration; antibody; hypertension; sincation related calcium regulated gene; HcZeKG; rat parathy extracellular calcium concentration; antibody; hypertension; sincation; sincation; value; rattus; incation/qualifiers Key Key Location/qualifiers Location (Qualifiers Aproduct Aproduct Aproduct Aproduct Aproduct Aproduct COSSAND; CO	V18890 standard; CDNA; 1100 BP. V18890 v18890 standard; CDNA; 1100 BP. V18891, O9-UUN-1998 (first entry) Rat Hypertension related calcium regulated gene; HCaRG; rat parathy, Hypertension related calcium regulated gene; HCaRG; rat parathy, extracellular calcium concentration; antibody; hypertension; sshpertension related calcium regulated gene; inflammatory disease; asthma. Rattus rattus. Location/Qualifiers Key 131.806 Atag= Arag= Ara
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V18891 standard; cDNA; 701

V18891

(first entry)

09-JUN-1998

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A (HAME/) HAMET P.

A (LEWA/) LEWANCZUK R.

A (TREM/) TREMBLAY J.

Gossard F. Hamet P. Lewanczuk R. Tremblay J.

Gossard F. Hamet P. Lewanczuk R. Tremblay J.

Hyp: 98-07171/07.

PT 98-07171/07.

PT reducts to treat or detect. e.g. hypertension, stroke, software tailure, cancer, diabetes or asthma or set oporosis, heart failure, cancer, diabetes or asthma or sequence gene (Hozago, which was isolated from the human parathyroid. This nucleic acid sequence encodes the hypertension related calcium regulated gene (Hozago, which was isolated from the human parathyroid. Its expression is regulated by extracellular calcium concentration. The sequence displays 75 percent homology to the rat form, with concerved areas such as the EF-hand like mocifs and the initiating concerved areas such as the EF-hand like mocifs and the initiating concerved areas such as the protein, can be used to detect or modulate (e.g. enhance or inhibit) abnormal calcium levels: They can specifically be used to detect or treat, e.g. hypertension, hyperthyroidism, osteoporosis, heart failure, diabetes, stroke, cancer, inflammatory disease, and asthma heart failure, diabetes, cancer, inflammatory disease, and asthma heart failure, diabetes, cancer, sequence 701 BP; 137 A; 204 C; 217 G; 139 T;
Human Hypertension related calcium regulated gene (HCaRG) ¢DNA.

Hypertension related calcium regulated gene; HCaRG; human parathyroid;
extracellular calcium concentration; antibody; hypertension; ss;
hyperthyroidism; osteoporosis; heart failure; diabetes; stroke;
cancer; inflammatory disease, asthma.
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I3-OCT-1996 (first entry)
Proliferation-inhibiting gene sequence.
Cell proliferation; cancer; viral infection; AIDS; HIV;
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23-JUN-1997; CA0439.
21-JUN-1996; US-667495.
(GOSS/) GOSSARD F.
(HAME/) HAMET P.
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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8888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a viral infection gene. The present invention describes nucleic acid sequences isolated from rat. The sequences of the invention comprise 70 viral infection (VI) genes and by tumour suppressor (TS) genes. Propagating cell cultures in the absence of the serum protein (SP) allows selective elimination of cells persistently infected with a virus from the cell culture. Inhibitors of the SP can be used for reducing or inhibiting a viral infection. Inhibitors of the TS gene products can be used to suppress a malignant phenotype (MP). The methods and inhibitors can be used with viruses such as similan immunodeficiency virus, avian immunodeficiency virus, bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             977 tataateteageeettggaagtetgaagetggaaatgggaagtgtaagetgggeetgge 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                Isolated human chromosome 4 fragment - used for therapy and diagnosis of cell proliferative disorders, e.g. cancer, AIDS, moles, warts and psoriasis.

Claim 4, Page 31a; 40p; English.

3 Human chromosome-4 fragments (T32033-35) comprise genetic determinants that are capable of inhibiting or arresting the proliferative capacity of a cell. They were identified using a microcell-mediated chromosome transfer protocol. The fragments are located at 4426-28 or 4433-34.1. They can be used in gene therapy of cancer and diseases, such as AIDS, that involve proliferative cells. They can also be used to diagnose the extent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1996; US-015334.
(UVVA-) UNIV VANDERBILT.
UDUOUS RN, Organ EL, Rubin DH;
WPI: 97-526456/48.
Genes involved in viral infection and tumour suppression - used to develop products for reducing or preventing viral infection or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1998 (first entry)
Viral infection gene SEQ ID NO:47.
Viral infection; tumour suppressor; cellular gene; rat; cancer; serum protein; inhibitor; malignant phenotype; HIV; influenza; hepatitis; retrovirus; immunodeficiency; ds.
Rattus sp.
W09739119-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
    mole; wart; psoriasis; chromosome 4; gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.8%; Score 41.4; DB 1; Length 218; 58.5%; Pred. No. 0.014; ive 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    55 T;
                                                                                                                                                                                                                                                                                                                                                                                                      63 G;
                                                                                                                                    Ning Y, Pereira-Smith OM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 64-65; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      31 C;
                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                             proliferative cells. They can and/or severity of malignancy. Sequence 218 BP; 69 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 849 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                26-JAN-1996; U01344.
26-JAN-1995; US-378289.
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11-APR-1997; U06067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            suppressing tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                          Bertram MJ, Ning
WPI; 96-362381/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aaa 1099
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Best Local Simi
Matches 72;
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V06127
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Example 2; Page 73-75; 127pp; English.

Example 2; Page 73-75; 127pp; English.

This is a murine interleukin-5 (IL-5) cDNA genomic fusion gene. This can this is a murine interleukin-5 (IL-5) cDNA genomic construct contain a chimeric pIL-5.ExpDNA sequence, comprising control sequence (TCS) and a segment encoding interleukin-5 (IL-5), which control sequence (TCS) and a segment encoding interleukin-5 (IL-5), which control sequence (TCS) and a segment encoding interleukin-5 (IL-5), which control sequence (TCS) are a segment encoding interleukin-5 (IL-5), which control is specific. The TCS is usually from a murine CD3delta gene. The chimeric Specific. The TCS is usually from a murine CD3delta gene. The chimeric CD NA sequence is integrated into the genome and causes IL-5 to be control integrated into the genome and causes IL-5 to be control least as models of IL-5 associated disease, e.g. asthma, eosinophilic used as models of IL-5 associated disease, e.g. asthma osinophilic pneumonia, myalgia, Loffler's syndrome, allergy, emphysema, pulmonary (Ibrosols, Wagener's granulomeatosis, adult respiratory distress syndrome (ARDS), bacterial or fungal infection, leukaemia, rheumatoid arthritis, atopic dermatitis or contact hypersensitivity, or to screen for IL-5 associated allergy managed and antiquial therapeutic agents for an IL-5 associated discontant and antiquial processing appendix agents for an IL-5 associated allergy managed and antiquial processing appendix agents for an IL-5 associated allergy managed and antiquial processing and appendix appendix and antiquial processing and appendix and antiquial processing and appendix appendix and antiquial processing and appendix and antiquial processing and appendix appendix and antiquial processing and appendix and antiquial antiquial processing and appendix and antiquial processing and appendix and antiquial antiquial processing and appendix and antiquial antiquial processing and appendix and appendix and antiquial antiquial antiquial antiquial appendix appendix and append
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                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1998 (first entry)
Murine II-5 cDNA genomic fusion gene.
Murine CD3delta: transcription control sequence; transgenic mouse; TCS;
T cell; interleukin-5; II-5; thymocyte; disease model; therapeutic agent;
screening; eosinophil; chimeric; fusion gene; ss.
Chimeric - Mus sp.
immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, caprine arthritis encephalitis virus or visna virus. Because the identified genes are non-essential to cell survival, the treatment methods can be used in subjects without serious detrimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      981 atctcagcccttggaagtctgaggctggagaatgggaagtgtaagctgggcctggcttc 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1844 AGGTAGATATGAAAGTTTGTGCTTATAAATAAAAAGAATATGAGAGTGGCAAATTATGTA 1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agoggaatttcaggttttgttttatgagtcaacagctgggcagggtggcacagtttata 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              998 tctgaggctggagaatgggaagtgtaagctgggcctggctttcatagtgaggctcagtg 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 regearrageaggaagruncregacaregritacarrieggrearcritaacaccrassag 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic mouse with interleukin-5 gene integrated into its genome under control of thymocyte and T cell, lung or basal keratinocyte specific regulator, useful as disease model or to screen therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       938 ttgttttatgagtcaacagctgggcagggtggcacagtttataatctcagcccttggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     752 GCTGAGAGAGGATCACAAGTTTAAGGCCTGACTGGGCTGCATNNTGAGATCCTGTG
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                                                                                                                                                                                                                                                                                                                                   Length 849;
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                                                                                                                                                                                                              216
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Pred. No. 0.79;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                               Score 39.8; DB 1;
Pred. No. 0.07;
0; Mismatches 51;
                                                                                                                                                                                                                  200
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50.98;
                                                                                                                                                                                                                                                                                                                                        3.6%;
ilarity 57.1%;
Conservative (
                                                                                                                                                                                                                      209 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T88014 standard; DNA; 6727
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89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1997; U05932.
09-APR-1996; US-629643.
(MAYO-) MAXO FOUNDATION.
                                                                                                                                                                                effects to the subjects Sequence 849 BP; 20
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97-512706/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee JJ, Lee NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9738086-A2.
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Best Local
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977 tataatctcagcccttggaagtctgaggctggagaatgggaagtgtaagctgggcctggc 1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding 25-hydroxyvitamin D 1-~a-hydroxylase .

Useful to detect and treat vitamin D related disorders
Example 4; Eage 77-79; 85pp; English.

This invention describes novel 25-hydroxyvitamin D 1-alpha-hydroxylase
(1-alpha-OHase), a renal cytochrome P450 enzyme of the vitamin D
pathway, and polynucleotides encoding the enzyme from human, mouse and
rat tissue. Molecules of the invention are used to diagnose and treat
Vitamin D-related disorders, to produce vitamin D metabolites, and to
identify modulators of the enzyme expression. The invention describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse 1-alpha-OHase promoter region DNA #1.

1-alpha-OHase; vitamin D 1-alpha-hydroxylase; vitamin D pathway;
renal cytochrome P450 enzyme; 25-hydroxyvitamin D; human; mouse; rat;
diagnosis; treatment; disorder; endocrine; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.1%; Pred. No. 1.2;
Matches 69; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1632 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1574 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1998; CA0758.
06-AUG-1997; US-906791.
(SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1201 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
X23315/c
ID X23315 standard; DNA; 4736 BP.
                               /number= 1
3764. .4555
/*tag= b
                                                                                                           /number= 2
5147. .5273
/*tag= c
/number= 3
5383. .5524
/*tag= d
/number= 4
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W09907835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a protein (sequence not given in the specification) which is expressed in malignant human tumours and their metastases. The DNA sequence has the potential to be a valuable probe for the accurate assessment of the prognosis of patients with malignant tumours, by examination of a tiny biopsy vample, or even a few cells obtd. by fine needle aspiration, and thus to influence therapy. No homology to any known coding regions was found using EMBL and Genbank databases. Three possible exons were predicted, one in the forward strand in frame 2 (between bases 55 and 942) and two in the forward strand in frame 2 (between bases 55 and 942) and two in the reverse strand, in frames 1 (between bases 55 and 942) and two in the RT-PCR technique to amplify homologous mRNA sequences from RNA extracted from metastastic human tumour cell lines (see 075271 and 079572-4).
1904 ATCCCAGTACTIGGGAGCCAAAGGCAGGGGTAGTCTGAGTCTAGGGCCAGCTTAGATACA 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          955 agctgggcagggtggcacagtttataatctcagccttggaagtctgaggctggagatg 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2075 AGCCGGGCGTGGTGGCCCTACTGTTAATCCCAGCACTCGGAAGGCAGAGGCAGGTT 2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1015 ggaagtgtaagctgggcctggctttcatagtgaggctcagtgtc----gaattaaagag 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2015 TCTGACTTTAGGCCAGCCTGGTCTACAAAGTTGAGTTCCAGAACAGCCAGGGCTACACAG 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                     10-501-1995 (first entry)
Unique 2.9 kb genomic DNA fragment from human metastatic tumour.
metastasis; cancer; tumour cell; probe; diagnosis; identification;
                                                     28-MAY-1997 (first entry)
Mouse cell cycle regulatory protein SPA-1 genomic DNA (exons 1-4).
Cell division cycle; Span-N; Span-C; lymphocyte differentiation;
mouse; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ner number to diagnosis or assessing the prognosis of tumour metastasis in patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 2858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
3.3%; Score 36.6; DB 1; Length 2.
Best Local Similarity 57.6%; Pred. No. 0.93;
Matches 87; Conservative 0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1070 gtaaagcaactattaaaaaaaaaaaaaa 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
3109. .3284
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human tumour metastasis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
T65001/C
ID T65001 standard; DNA; 5687 BP.
AC T65001,
DT 28-MAY-1997 (first entry)
DE Mouse cell cycle regulatory prote
KW Cell division cycle; Span-N; Span
KW mouse; murine; ds.
OS Mus sp.
FH Key 3109, 3284
FT exon 3284
FT
                                                                                                                                                                                                                                     075270 standard; DNA; 2858 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAY-1994; G01160.
28-MAY-1993; GB-011130.
(ISIS-) ISIS INNOVATION LTD.
TATIN D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 14-15; 22pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 95-022801/03.
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
WO9428129-A.
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Human secreted protein; fusion protein; gene therapy; protein therapy; diagnosis, tissue, cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; diffaumation; stochma; lymphocytic disease; brain; hepatic; lymphom; immune system; asthma; lymphocytic disease; brain; hepatic; lymphom; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
human
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                                                                                                                                                                                                                                                                                                                                                                                acagctgggcagggtggcacagtttataatctcagcccttggaagtctgaggctggagaa 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                   4479 ACAGCTGGAAGTGGTAGCTCAAGTCTGTAACCCAATACTTGGGAAGGTGAGGCAAGGAGG 4420
                                                                                                                                                                                                                                                                                                                               Gaps
an animal cell transformed with the enzyme promoter which is used to identify compounds which modulate activity of the polynucleotide encoding the enzyme, and to modulate the production of vitamin D in patients with vitamin D endocrine disorders in the vitamin D hydroxylation pathway, the enzyme catalyses conversion of 25-hydroxyvitamin D to 1 alpha 25(GH)2D3.
Sequence 4736 BP; 1061 A; 11375 C; 1160 G; 1140 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders Claim 1; Page 214; 312pp; English.

This sequence represents a nucleic acid molecule which encodes a sechuman protein. The gene number is given in the descriptor line. The can be used to generate fusion proteins by linking to the gene to a
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                                                                                                                                                                                                                                                                     DB 1; Length 4736;
                                                                                                                                                                                                                                                                                                                            51; Indels
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Moore PA, Rosen CA, Ruben SM, Shi Y, Wei Y,
                                                                                                                                                                                                                                                                                           Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                                                                                                  Score 36.4;
                                                                                                                                                                                                                                                                  3.3%;
56.8%;
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                                                                                                                                                                                                                                                            Query Match 3.3
Best Local Similarity 56.8
Matches 67; Conservative
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US-054212.
US-054213.
US-054214.
US-054215.
US-054215.
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US-055969.
US-055972.
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19-AUG-1997; US-0567
30-JUL-1997; US-0542
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Carter KC, Endress
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WO9906423-Al
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immunoglobulin Fc portion (e.g. X20403) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 83 novel genes and their fragments (nucleic acid sequences: X20412-X20499; amino acid sequences Y00258-Y00377) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see X20412 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Behaouah A, Shaphro SD;

Belaouah A, Shaphro SD;

Relaouah Shaphro SD;

Rela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse neutrophil elastase gene promoter.
Neutrophil elastase; mouse; transgenic animal; knockout animal;
emphysema; cystic fibrosis; infection; animal model; promoter; ds.
Mus musculus strain 129/SvJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane conductance regulator. They can also be used as models for disorders such as pulmonary emphysema and for the role of NE in combating infection. The promoter of the NE gene can be used for studying the regulation of the gene, or in studies where targetting of gene expression to neutrophils is desired. Sequence 1371 BP; 352 A; 303 C; 339 G; 377 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                            152 G;
                                                                                                                                                                                                                                                                                                                                                                                                             3.3%; Score 36.2; DB
62.9%; Pred. No. 0.63;
tive 0; Mismatches
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                            133 C;
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30-MAR-1998; U06266.
27-MAR-1999; US-042279.
31-MAR-1997; US-042871.
(BARN-) BARNES-JEWISH HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%;
                                                                                                                                                                                                                                                                                                                            194 A;
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ID v33755 standard; DNA; 1371
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nes 76; Conservative
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                         602 BP;
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'note= "Motif with the potential to form Z-DNA
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/label= GIRE,Myc
/note= "Transcription factor binding site"
640. 647
/label- p53
/note- "Transcription factor binding site"
208. .220
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/note= "Transcription factor binding site"
2045. .2051
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/label= Myb
/note= "ranscription factor binding site"
453. .459
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322. .327
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fnote= "Transcription factor binding
1291, 559
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/label= HNF-5
/note= "Transcription factor binding
004. .523
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/note= "Transcription factor binding
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note- "Transcription factor binding
037. .1043
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label= HNF-5
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634. .1640
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/label- Ap-1
1816. 1874 Inding
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|41. .746
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                                   2743 AGGCTAAGGTGGGATGATCATAAGTTTGAAGCTAGCCTAGGGCACATAACAAGTCTCAGA 2802
 934 TITAACCCCAGCACTCGGGAGGCAGGCAGGCAGGTTTCTGAGTTCGAGGCCAGCCTGG 875
                                                            Gaps
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AS-30D tumour Type II hexokinase 4.3kbp proximal promoter region.
Response element; Z-DNA; neoplasia; hexokinase II; glycolysis; cancer; gene therapy; diabetes; tumour; rat; ds.
Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repressing agent
The polypetide encoded by this sequence (and derivatives having annino acid substitutions, additions or deletions) may be used as anticancer/tumour repressing agent.

Sequence 2851 Bp: 745 A; 674 C; 660 G; 769 T;
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(AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
(ROHT-) ROHTO SEIYAKU KK.
WPI; 94-328995/41.
P-PSDB; R62634.
NOVel DA encoding a peptide - useful as an anticancer, tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 3.3%; Score 36.2; DB 1; Length 2851; Best Local Similarity 59.0%; Pred. No. 1.2; Matches 62; Conservative 0; Mismatches 43; Indels 0
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/label= p53
/note= "Transcription factor binding site"
1711. .180
/*tag= c
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/label- Myb
/note= Transcription factor binding site"
118. .126
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                                                                                                                                                                                                                                                                                                                                                10. .411
/*tag= a
/product= Anticancer polypeptide
                                                                                                                                                                                                                                                                              Cancer repression gene.
Cancer; anticancer agent; tumour repression; ss.
Mus musculus.
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10. .411
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03-MAR-1993, 069231
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T78598
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Q72975
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/tag- ad
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/tag- ae
/label- NF-IL6,Ap-1
/note- Transcription factor binding site"
/tag- af
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/note- Transcription factor binding site"
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Tabel= Ap-1

Note= "Transcription factor binding site"

7553. 2636

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77pt_type= DIRECT
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|abel= 8p-1
|note= "Transcription factor binding site"
165. .2171
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|Tabel- HNF-5
|Abel- Transcription factor binding site
| 325. .232
|*tag= z
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|Jabel- Ap-2
|note- "Transcription factor binding site"
|413. _2420
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note= "Transcription factor binding
402. .2409
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abel= I
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*tag= w
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V05159;
20-dru-1998 (first entry)
Mouse butyrophilin gene.
Butyrophilin; btn gene; promoter; mouse; transgenic animal;
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                         /tag- an /label- Myb /note- Transcription factor binding site" 3233. .328 /*tag- ao /label- SRE /note- Transcription factor binding site" 3256. .3267 /*tag- ap /label- Sp-1,Ap-2,SRE /note- Transcription factor binding site" 3306. .3313 /*tag- aq /label- c/ebp /note- Transcription factor binding site" 3352. .3360 /*tag- ar /label- NF-IL6 /note- Transcription factor binding site" /label- NF-IL6 /note- Transcription factor binding site" 3450. .3360 /*tag- as /rpc_type- DIRECT /label- II 3492. .3509 /*tag- at /label- II 3492. .3509 /*tag- at //tag- at //
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/label- Ap-2
/note- "Transcription factor binding site"
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/evidence= EXPERIMENTAL
/standard_name= transcription start site
/note= "most frequently used site"
4645, .4651
/*tag= d
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3.3%; Score 36.2; DB 1;
Best Local Similarity 60.8%; Pred. No. 1.5;
Matches 59; Conservative 1 0; Mismatches 38;
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1. .4693
/*tag= a
/note= "Claim 4"
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'label= III
1507. .3513
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V05159.

AC V05159,
DT 20-UUL-1998 (first entry)
DE Mouse butyrophilin gene.
KW Butyrophilin, btn gene; promoter;
KW GS.
OS Mus musculus.
FT Key Location/Qualifier
FT Promoter 1.469° a /*tag a /*tag b /*tag b /*tag b /*tag b /*tag fT Prim_transcript 4611 /*tag b /*tag FT FT Prim_transcript 4611 /*tag b /*tag fT /*ta
protein_bind
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/*tag- /number intron 9636 /*tag- /evider /umber	exon 1	exon 1		FT repeat_unit 48074814 FT /*tag= af /*tag= af /*tag= INVERTED FT repeat_unit 1255612563 FT repeat_unit 14559	protein_bind	protein_bind compler /*tag- /note- protein_bind compler	protein_bind	protein_bind	protein_bind 3129. /*tag=/rag=protein_bind 3132. /*tag=/rag=/rag=/rag=/rag=/rag=/rag=/rag=/r	protein_bind 3139. /*tag-/rtag-/note- protein_bind _compler	FT / reag = ap / reag = ap / reag = ap / reag = ag FT protein_bind 3181. 3189	/*tag= ar /note= "C/EBP" protein_bind 31903195 /*tag= as /note= "PU.1"	protein_bind compler /*tag-
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misc_signal misc_signal	misc_signal misc_signal	prim_transcript	T prim_transcript T T T T T T T PolyA_signal	prim_transcript	CDS	sig_peptide CDS	CDS	CDS	CDS	exon	intron	intron	exon intron exon

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Human secreted protein constanting gene 10.

Human secreted protein treatment; prevention; protein therapy; AIDS; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia; cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis; arthritis; malignancy; digestive; endocrine; infection; ss.
                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. neurological disorders, turnaurs, inflammation or haematological disorders, turnaurs, inflammation or haematological disorders, turnaurs, immune disorders, inflammation or haematological disorders, claim 1; Page 169; 215pp; English.

X51701-55 encode human secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the presence of mutations in the new polynucleotides. Specific uses are described for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, autoimmune disorders, tumours, atherosclerosis, restenosis, autoimmune disorders, inducers, neurological disorders, arthritic disorders, skeletal disorders, neurological disorders, arthritic clisorders, skeletal disorders, neurological for identifying their rejection. The polypeptides are also useful for identifying their binding partners.
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                                                                                                                  Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen GA, Ruben SM, Shi Y; WPI; 99-204988/17.
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                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity
Matches 49; Conservat
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WO9918208-A1.
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01-OCT-1998;
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02-0CT-1997;
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DNA encoding a human serieted protein.

Inflammatory disorder; skin disorder; tumour; atherosclerosis;

restenosis; autolimmune disorder; Alzheimer's disease;

peripheral neuropathy; trauma; spinal cord injury; allergy;

hematopoietic disorder; skeletal disorder; neurological disorder;

arthritic disorder; skeletal immunodeficiency disease; AIDS;

transplant rejection; ss.
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ilarity 53.1%; Pred. No. 2.3;
Conservative 0; Mismatches 68; Indels 0;
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/note= "alpha-INF"
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New isolates unuan genes and the secreted polypeptides lury encoue Claim la; page 232-233; 168pp; English.

Claim la; page 232-233; 168pp; English.

Co This invention describes novel isolated human genes and the secreted content of the encoder. The products of the invention are useful for mean profuse and encoder in the encoder of preventing, treating or ameliorating medical conditions, e.g. by protein conferentially the amount of the new polypeptides in a sample or by conferentially the presence of mutations in the new polynucleotides. Based on Specific uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal contromed diseases, blood disorders, leukemias, diseases of the immune system, autorimmune diseases, hepatic and renal diseases lymphomas, inflammation, allergies, Alzheimer's and cognitive disorders, pulmonary disorders, transplant rejection, disorders involving osteoclasts such as costeoporosis, arthritis or malignancies, diseases, such as contains and products of the invention are represented in X07852-X07993 and the encoding nucleic acids are represented in X37451-X37552.
                                                                                                           New isolated human genes and the secreted polypeptides they encode
Florence KA, Greene JM, Janat F, Lafleur DW, Ni J,
Rosen CA, Ruben SM, Shi Y, Young P, Yu G;
                          Rosen CA, Ruben SM
WPI; 99-264022/22.
P-PSDB; Y07861.
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ö 1030 gcctggctttcatagtgaggctcagtgtcgaattaaagaggtaaagcaactattaaaaaa 1089 0; Gaps Query Match 3.2%; Score 35.4; DB 1; Length 1089; Best Local Similarity 69.6%; Pred. No. 1.4; Matches 48; Conservative 0; Mismatches 21; Indels 0; g à

1090 aaaaaaaa 1098

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Search completed: May 15, 2000, 01:45:56 Job time: 9820 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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	AF124523 Homo sap	AF124523 AF124523	HTG. human.	Eukaryot Eutheria	<pre>1 (base Schudy, P Merck-Ro</pre>	Direct Submitte			repeat_region	action teador			repeat_region	repeat_region	repeat_reqion		repeat_region	repeat_region	repeat region		repeat_region				repear_regrou	repeat_region	repeat_region	repeat_region
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/note="mink acc.no. M29580"
/product="ZFP7"
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/evidence=not_experimental
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4129. 4159
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4623. 4196
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/note-"homology = 100.00%, score = 26,
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/evidence-not_experimental

11725. .12006

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/rpt_family="Alux"
4104. .4431
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Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 17492)

Schudy, A., Schilhabel, M., Baumgart, C., Menzel, U., Weber, J.,

Schattevoy, R. and Rosenthal, A.

Direct Submission

A. Submission

Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

1-75864, config of 1864 bp; 75864-75865; app of unknown size;

78865-109038: contig of 18784 bp; 109038-109039: gap of unknown size;

78865-109038: contig of 1830 bp; 117368-117369: gap of unknown size;

134145-134146: gap of unknown size; 128689-134145: contig of 5457 bp;

134145-134146: gap of unknown size; 14460-1149478: contig of 1858 bp; 149478-149479: gap of unknown size; 14762-149478: contig of 1858 bp; 149478-149479: gap of unknown size; 149479-15177:

151778-155130: contig of 333 bp; 155130-155131: gap of unknown size;

155111-155254: contig of 2124 bp; 157254-157255: gap of unknown size; 155111-157254: contig of 1238 bp; 158492-188493: gap of unknown size;

1840 of unknown size; 157855-158492: contig of 1238 bp; 1531292-188493:
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                              264 aggagcaccttcagaaagttgttgaaacttgtagtcgggggccctgcatgggaaagactgc 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    683
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                                                                                                                    324 agagaagctgtggagcaacttggtgccagcgccaacctgtcagaagagcgtctggccgtc
                                                                                                                                                                                                                                                                                                                             36954 AAGCCIGACACCTICAGGACCAGCICCAGGAGCTCTGCATCCCCCAAGACCTGGTCGGG
                                                                                                                                                                                                                                                                                                                                                                                           384 ctgctggcgggcacacacaccctgctccagcaggctctccggctgcccctgctagtcta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cagggatcctcgctgcctcacgtgtcttacttccggtggcgggtggacgtggccatctca
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/gene="zinc-finger protein 7 (2FP7)"
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//TEERS LATE OIS WERVETED VAN HES REEW OCLD PO GRALY REVILENHES SVAGLA
GFLVFR PELLS RLEQGEE WYLDLOGARGTEAPRISKTDSTIRTENEDACED MILLS
GFLVFR PELLS RLEQGEE WYLDLOGARGTEAPRISKTDSTIRTENEDACED MILLS
FYTRD ADGOGKELGS SOCLOCOPES SOWLDS HAVE FRONK CLECK TRATSDIALHWEIN
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SSSLIYHQRIHKGEKPYECLQCGKAFSMSTQLIHQRYHTGERPYKCNECGKAFSQNS
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KKVNIIKKLHQCEDCEKIFRWRSHLIIHQRIHTGEKPYKCNDCGKAFNRSSRLIQHQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="homology = 74.10%, score = 20, counts = 9" /rpt_type=tandem
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                                                                  15811. .15858
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Pred. No. 7.6e-126;
0; Mismatches 168;
                                                                                                                                                                                                                       /product="zinc-finger protein 7"
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18270. .18401
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complement(19740. 20031)
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/rpt_family="LIM4"
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Best Local Similarity 77.3%;
Matches 572; Conservative
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8046. .9818
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/evidence=not_experimental
8046. .9818
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/note="GENCGAN"
complement(12368. .12424)
/note="Text of the complement of the complem
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/evidence=not_experimental
14715. .14969
/rpt_fami@y="AluJo"
15002. .15162
                                                                                                                                                                                                                                                                                      /evidence=not_experimental 9299. .9578 /rpt_type=tandem 9958. .10259 /rpt_family="Alux" complement(10113. .10232)
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/ rpt_family" MERS8B"
1334. 13491
/ rpt_type=liverted
complement(13354. 13641)
/ rpt_family" Alux"
13949. 14111
/ rpt_family" FRAM"
14263. 14357
/ rpt_family" L2b"
complement(14534. 14650)
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11078. 11384
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11359. 11384
/rpt_type=tandem
11519. 11638
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complement(11792. 11848)
/rpt_family="LTR40b"
complement(11834. 11860)
                                        /evidence=not_experimental
8005. .9818
/note="GENSCAN"
8046. .9818
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/evidence=not_experimental
10238. .10259
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complement(12673. .12773)
/note="GRAIL"
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2872. .12961
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2985. .13069
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15168. 19812
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16383. 16634
/rpt_family="L2"
/1575. 16831
/note="GRAIL"
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15022. .15161
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NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
complement(457. .748)
/rpt_family="Alusg"
complement(750. .820)
/rpt_family="Ling-orf2"
complement(1167. .1754)
/rpt_family="Lind-orf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental complement(4603. .5038) /rpt_family="MLrlC" complement(4836. .4889) /note="GRALL"
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/evidence=not_experimental
complement(5199. .5235)
/note="MZEF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1387. .1410
/rpt_type=tandem
complement(1410. .1713)
/rpt_family="Alux"
1434. .155
/note="FEXHB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="BAC 704B241056"
complement(36.349)
/rpt_family="AluSx"
352. .405
/rpt_type=tandem
complement(449. .582)
/note="FEXHB"
                                                                                                                                 /organ.tsm="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2738. .3017
/rpt_family="AluJo"
2747. .2931
/rpt_type=inverted
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3369. 3458
/note="GENSCAN"
/note="GENSCAN"
/note="GENSCAN"
/note="GENSCAN"
/note="MZEF"
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- -0.43%, comment = Initial_exon 108
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                                  /hote="GenScan, score = 0%, comment = P2_471_aa GENSCAN predicted peptide is unknown ->NN (DEF2) prediction for sec struc composition: all beta sheet; overall class:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="hypothetical"
/note="GenScan, score = 0.51%, comment = Internal_exon
bp frame: 0 phase: 2"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26797. .26852
/gene="hypothetical"
/note="GenScan, score = 0.81%, comment = Internal_exon
bp frame: 1 phase: 2"
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (28-ARR-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
Location, Qualifiers
                                                                                                                                                                                                  AF146367 69528 bp DNA PRI 20-MAY-1999
Homo sapiens chromosome 8 PAC PSA4.00 containing gene for zinc
                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6528)
Rump,A., Schudy,A., Drescher,B., Koczan,D., Thiessen,H.-J.,
Merck-Roussau,M.-F. and Rosenthal,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /hote="GenScan, score = 1186%, comment = Pl_377_aa of owl|Pl5622|ZF64_HUMAN ZINC FINGER PROTEIN CLONE (FRAGMENT). - HOMO SAPIENS P = 1.2e-120 S = 1186"
                 744 gccttggtccttaaggagatggcagaactggagaagtatgagcgcaaactgcaggac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20121. 20134
/gene="hypothetical"
/note="GenScan, score = 0.84%,
bp frame: 0 phase: 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence-not_experimental
9896. .1003
/gene="hypothetical"
/note="GenScan, score = -0.4
bp frame: 1 phase: 0"
/evidence-not_experimental
20029. .20039
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26797. .26852
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27802. .27935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .69528
/organism="Homo saplens"
/db_xref="taxon:9606"
/chromosome="8"
/clone="PAG P5A4.00"
5504. .6988
/gene="hypothetical"
                                                                                                                                                                                                                    Inger protein, complete sequence.
AF146367
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/gene="hypothetical"
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                                                                                                          17317 TGACCCCTCACTTGACCAGT 17298
                                                                                    823
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                                                                                    tgactgaaccctggtactgt
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KEYWORDS
SOURCE
ORGANISM
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llarity 77.3%; Pred. No. 7.9e-126;
Conservative 0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
17537. .17863
/note="GRAIL"
/evidence=not_experimental
complement(18086. .18181)
                         /rpt_family="L2a"
16722. 16761
/rpt_family="L2b"
16782. 16912
/rpt_family="L2a"
complement(17315. 17989)
evidence=not_experimental
                                                                                                                                              /evidence=not_experimental complement(17315. .18046)
                                                                                                                                                                                                                           /evidence=not_experimental complement(17338. .17681)
                                                                                                                                                                                                                                                                           /evidence-not_experimental
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                                                                                                                                                                         /note="GENSCAN"
                                                                                                                                                                                                            /note-"XPOUND"
            .16761
                                                                                                                                                                                                                                                                                         17351. .17527
/note="GRAIL"
                                                                                                                                                                                                                                                              /note-"MZEF
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Matches 572; Conserv
             repeat_region
                                            repeat_region
                                                                              repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comment - Internal_exon 117
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                                                                                                         comment - Internal_exon 117
                  134
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                                                                                                                                                                                                                                                                                                                                                                                       /note="GenScan, score = 113.55%, comment = Terminal_exon 1814 bp frame: 2 phase: 2" /evidence=not_experimental complement(50641. .50757)
                                                                                                                                                                                            /note="GenScan, score = 71.21%, comment = Terminal_exon /732 bp frame: 0 phase: 0. /evidence=not_experimental complement(44951. .60537)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36886 TTGGGGGCCCAGCTTCCTCCAGAGGTGGCAGCAATGGCCCGGCTACTAGGGGGACCTAGAC 36945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37006 CGAGAGGCTGTGCAGCGTCTTGGGGTCAGCGCCAACCTGCCGGAGGAGCAGCTGGGTGCC 37065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34766 TCTGGGACCGACCTCCTGGGCTGGTGATCAAAGAGGAAGCAGCAGCAATGTCTGCTGTG 36825
                - 4.67%, comment - Internal_exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comment - Internal_exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggagcacetteagaaagttgttgaaaettgtagteggggeeetgeatgggaaagaetge 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgtggttaggaccttctcttcggactggtcaagaaacgggaagaaaggatgtctgctttg 143
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llarity 77.0%; Pred. No. 6.2e-125;
Conservative 0; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="GenScan, score = 10.62%,
bp frame: 1 phase: 2"
                                                                                                         /note="GenScan, score = 0.77%, op frame: 2 phase: 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="GenScan, score = 7.44%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="GenScan, score = 1.36%, bp frame: 2 phase: 0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence-not_experimental
18304 c 16802 g 16922 t
                                                                                                                                        /evidence=not_experimental
36757. 37488
/gene="hypothetical"
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                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental complement(44982. .46795)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp frame: 1 phase: 0"
/evidence=not_experimental
complement(51365, .51454)
                                                       /evidence=not_experimental
/gene="hypothetical"
/note="GenScan, score
op frame: 2 phase: 2"
                                                                      31554. .31670
/gene="hypothetical"
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complement(2184. .2219)
/note="Exon predicted by several exon prediction programs and by homology to GenBank entry HUMZIFIA_1: Homo sapiens and finger protein mRNA, 3' end."
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37186 GACTIGGCCAGCGIGGIAITIGGGAGCCAGCGGCCCCICCTIGAITCIGIGGCCCAGCAG 37245
                                                                                                                                                                                                                                                                                                                37246 CAGGGGGCCTGGCTGCCGCATGTTGCTGACTTTCGGTGGCGGGTGGATGTAGCAATTTCC 37305
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8qter PAC clone P2G2, complete sequence.
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1 (bases 1 to 128009)

Rump, A., Rosenthal, A., Drescher, B., Weber, J., Schattevoy, R., Koczan, D., Thiesen, H.-J. and Merck-Rousseau, M.-F.

Direct Submission
Submitted (08-JAN-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
Location/Qualifiers
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                                                                         aagccagatgccttccaggaagagctccaggaacttggcattcctcaggatctaattgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gccttggtccttaaggagatggcagaactggagaagaagtgtgagcgcaaactgcaggac
                                                                                                                                                                                                                                                                     cagggatectegetgeeteaegtgtettaetteeggtggegggtggacgtggecatetea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggatctgcacaccgcttcgaggtgcccatagccaaatttcaggagctgcggtacagtgta
                                                                                                                                                                        gatttggccagtttggcatttgggagtcaacgccctcttctcgactctgtagcccaacag
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//note="Exon predicted by several exon prediction and by homology to GenBank entry HUMZNFN 1: Homo DNA-binding protein (ZNF) gene, partial cds."/evidence=not_experimental
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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53

Vertebrata; Mammalia;

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collymar, C., Collymore, A., Cooke, P., Catllano, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Rano, E., Radora, A., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Heboczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vasailiev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Meeler, J., Wu, X., Direct, Submission
                                                                                                                                                                                     ACO11951 133200 bp DNA HTG 13-DEC-1999
Homo sapiens clone RP11-18M17, *** SEQUENCING IN PROGRESS ***, unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-OCT-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 10, 1999 this sequence version replaced gi:6056232. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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gap of unknown length
1130: contig of 89 bp in length
2412: contig of 1282 bp in length
gap of unknown length
3457: contig of 1045 bp in length
gap of unknown length
4573: contig of 1116 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
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unknown length
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 133200)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-18M17
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                               804 tgactgaaccctggtactgt 823
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HTG; HTGS_PHASE1.
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KEYWORDS
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                                         ŏ
  and by homology to GenBank entry HSKOX9_1: Human Kox9 mRNA for zinc finger protein, partial."

/evidence=not_experimental
47430. 47631

/note="Exon predicted by several exon prediction programs and by homology to GenBank entry AF024700_1: Homo sapiens clone B4-2 zinc finger protein mRNA, partial cds."
/evidence=not_experimental
94802. 95455

/note="Exon predicted by several exon prediction programs and by homology to GenBank entry HSZFP647_1: Human mRNA for zinc finger protein (clone 647)."
/evidence=not_experimental
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HSKOX9_1: Human Kox9 mRNA
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and by homology to GenBank entry HSZNFPT7_1: H.sapiens
mRNa for Zinc-finger protein (ZNFPT7)."
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8 85984: 2 92357: 8 9572: 3 99411: 2 103446: 7 108787: 108787: 0 124476: 1 133200: 1 13320	38.0%; 77.2%; vative	iggetgeaget 	egggtteceae GGGGGCCCAC	gagcacctto	gcagagaagctgte 	cctgctggcgggg ccracregcagg	cagatgo CCAACAO	agatttggccagttt GGACTTGGCCAGCGI	cagggateetege 	cagogotoagi cagigocotigo	cagatggatctgcacac
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E thera: primates: Catarrhin; Hominidae; Homo.

E (bases 1 to 1588)

L Ondy, H., Ren, S., Huang, C., Jiang, C., Li, Y., Zhou, J., Yu, Y., Xu, S., Wang, Y., Fu, G., Chen, Z. and Han, Z.

L One, H., Ren, S., Huang, C., Jiang, C., Li, Y., Zhou, J., Yu, Y., Xu, S., Unbublished

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D Ong, H., Ren, S., Huang, C., Jiang, C., Li, Y., Zhou, J., Yu, Y., Xu, S., Wang, Y., Fu, G., Chen, Z. and Han, Z.

Direct Submission

L Submitted (16-DEC-1998) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Rd., Zhangjiang Hi-Tech Park, Pudong, Shanghai, 201203, China

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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Homo sapiens hypothalamus protein HT002 mRNA, complete cds.
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/protein_id="AAF14877.1"
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Pred. No. 5.6e-109;
0; Mismatches 174;
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/tissue_type="hypothalamus"
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Homo sapiens chromosome 5 clone CIT-HSPC_235N22, WORKING DRAFT
SEQUENCE, 27 unordered pieces.
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Eutheria; Frinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 78543)
DOE Joint Genome Institute.
                                                  agatttggccagtttggcatttgggagtcaacgcctcttctcgactctgtagcccaaca
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HTG: HTGS_PHASE1; HTGS_DRAFT
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DOE Joint Genome Institute.
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Mammalia;

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AC007636 78651 bp DNA ROD 15-FEB-2000
Mus musculus chromosome 6 clone unknown strain RIII Fibroblast cell
11ne C127, complete sequence.
                                                                                                                                                                                                                                                                                              Submitted (1-MAY-1999) Department Of Chemistry And Blochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, 67 31019, USA.

3 (bases 1 to 78651)

Yao,Z., Shual,S., Wu,H., Meisler,M. and Roe,B.A.

Blacet Submission

Submitted (03-FEB-2000) Department Of Chemistry And Blochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                 Yao,z., Shual,S., Wu'H., Meisler,M. and Roe,B.A.
Direct Submission
Submitted (LDF-FEB-2000) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman.
TCTGAGTTCAGGCCAGCCTGGGCTATACAGAAAACCCTGTCTCAAAAAAACCAAAAAAA 39409
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Feb 3, 2000 this sequence version replaced gi:6730773.
I.ortion/Qualifiers
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Mus musculus Chromosome 6 PAC Clone pl_4 In MND2 Region
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 78651)
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| 20258 c 18946 g 18526 t
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2 (bases 1 to 78651)
Yao, Z., Shual,S., Wu,H., Meisler,M. and Roe,B.A.
Direct Submission
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gap of unknown length
41428: contig of 2217 bp in length
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45655: contig of 4227 bp in length
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/db_xref="taxon:9606"
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Query Match
4.6%; Score 50.2; DB 12; Length 78651;
Best Local Similarity 59.4%; Pred. No. 0.0015;
Matches 85; Conservative 0; Mismatches 58; Indels 0;
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Sutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AC007306 78783 bp DNA ROD 15-FEB-2000
Mus musculus chromosome 6 clone unknown strain RIII Fibroblast cell
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OK 73019, USA
ON Feb 11, 2000 this sequence version replaced di:6691340.
                                                                                                                                                                                                                                                              2 (bases 1 to 78783)
Chen,F., Do,T., Do,A., Meisler,M. and Roe,B.A.
Direct Submission
Submitted (14-APR-1999) Department of Chemistry And Biochemistry,
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Submitted (10-FEB-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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Chen,F., Do,T., Do,A., Meisler,M. and Roe,B.A.
Direct Submission
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sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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1 (bases 1 to 138608)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus chromosome 11, clone RP23-199H17
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"S Dasses I to 167859)
"S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavki, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fizhugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, M.,
Deterson, R., Pollara, V., Riley, R. Roy, A., Santos, R., Severy, P.,
Feterson, K., Pollara, V., Riley, R., Santos, R., Severy, P.,
Frespace Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Wyman, D., Ye, W., J., Zimmer, A. and Zody, M.,
Direct Submission
Submitted (14-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 17, 2000 this sequence version replaced gi:6730840.
Shit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Center
Center: Whitehead Institute/ MIT Center for Genome Center
       Mammalia;
Mus.
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Center clone name: 450_A.18

Sequencing vector: M13; M77812; 100% of reads
Sequencing vector: M13; M77812; 100% of reads
Chemistry: Dye-terminator Big bye: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152833 bases at least 040
Consensus quality: 165208 bases at least 030
Consensus quality: 164488 bases at least 030
Insert size: 181000; agarose-fp
Insert size: 187895; sum-of-contigs
Quality coverage: 3.1 in 020 bases; sum-of-contigs
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 167859)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5030
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gap of unknown length
contig of 1073 bp in length
gap of unknown length
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                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-450A18
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Web site: http://www-seq.wi.mit.edu
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                                   REFERENCE
AUTHORS
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JOURNAL
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Db 117520 TITCAAGAGACCTAAACTGGGTGTGATGGCACAGACCTGCAATCTCAGCACTTGGATGGC 117579
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Mus musculus chromosome 10 clone RP21-522L13 map 10, LOW-PASS
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64.9%; Pred. No. 0.0053;
iive 0; Mismatches 46; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                          of 8876 bp in length

Jap of unknown length

Jud9: contig of 8637 bp in length

gap of unknown length

120462: contig of 10980 bp in 1

131928: contig of 11;

148037:
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1. 167859
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="irp23-456A18"
/clone=lib="RPDI-25"
#8301 a 36172 c 36115 g 47258 t 13 Others
                                                                             gap of unknown length
contig of 2601 bp in length
gap of unknown length
contig of 3053 bp in length
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contig of 19822 bp in length
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Best Local Similarity 64.99
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AC015891
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contig of 864 bp in length gap of unknown length contig of 832 bp in length gap of unknown length contig of 862 bp in length gap of unknown length gap of unknown length contig of 852 bp in length gap of unknown length contig of 852 bp in length gap of unknown length contig of 897 bp in length gap of unknown length contig of 897 bp in length gap of unknown length contig of 830 bp in length gap of unknown length contig of 839 bp in length gap of unknown length contig of 839 bp in length gap of unknown length contig of 835 bp in length gap of unknown length gap of unknown length contig of 895 bp in length gap of unknown length gap of unknown length contig of 895 bp in length gap of unknown length contig of 895 bp in length gap of unknown length contig of 895 bp in length gap of unknown length contig of 895 bp in length gap of unknown length contig of 893 bp in length gap of unknown length gap of unknown length contig of 893 bp in length gap of unknown length gap of unknown length contig of 895 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 895 bp in length gap of unknown length contig of 895 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 893 bp in length gap of unknown length contig of 893 bp in length gap of unknown le
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unknown length
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E 2 (bases 1 to 230475)

E 2 (bases 1 to 230475)

E 3 (bases 1 to 230475)

E 3 (bases 1 to 230475)

E 4 (bases 1 to 230475)

E 5 (bases 1 to 230475)

E 6 (bases 1 to 230476)

E 7 (bases 1 to 230476)

E 8 (bases 2 to 2000 to
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 230475) Blaren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 10, clone RP21-522L13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This record contains 279 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Center clone name: 522_L_13
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musculus clone RP21-82116, WORKING DRAFT SEQUENCE, 80 unordered
                                                                                                                                                                                                   Unpublished

2 (Pases 1 to 23854)

DOE Joint Genome Institute.

Direct Submission

Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                     web site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 160205 bases at least Q40
Consensus quality: 1206026 bases at least Q30
Consensus quality: 238602 bases at least Q20
Stimated insert size: 238554; sum-of-contigs estimation
Estimated insert size: 162000; pulse field gel estimation
Quality coverage: 4.94x in Q20 bases; pulse field gel estimation
Quality coverage: 3.36x in Q20 bases; sum-of-contigs estimation
                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23854)
DOE Joint Genome Institute.
Sequencing of Mouse
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RESULT 14 AF213391

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AGSVTLDGHDLRTLNPSWLRGQVIGFISQEPVLFATIMENIRFGKLDASDEEVYTAA
REANAHEFISSFHDGYSTVVGWDPRRTP"
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                                                                                                                                                      1 (Mases 1 to 963)
Schriml, L. M. and Dean, M.
Identification of 18 mouse ABC genes and characterization of the ABC superfamily in Mus musculus
Unpublished
C pases 1 to 963)
Schriml, L. M. and Dean, M.
Direct Submission
Submitted (09-DEC-1999) Laboratory of Genomic Diversity, National Cancer Institute, FCRDC, P.O. Box B, Frederick, MD 21702-1201, USA
Location/Qualifiers
1. 963
AF213391 963 bp mRNA ROD 07-FEB-2000 Mus musculus AFP-binding cassette protein (Abcb8) mRNA, partial
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 (bases 1 to 7218)

Dorner,F., Schelflinger,F. and Falkner,F.Gunter.

Recombinant fowlpox virus

Patent: US 5670367-A 14 23-SEP-1997;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6JxDBA"
/db_xref="taxon:10090"
/note="sub-family B; MDR member 8"
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Best Local Similarity 57.2%; Pred. No. 0.019;
Matches 83; Conservative 0; Mismatches 62;
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Sequence 14 from patent US 5670367.
166494.1 GI:2724471
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                     Homo sapiens hypothalamus protein HT002 mRNA, complete cds. AF113540.1 GI:6523834
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Dong, H., Ren, S., Huang, C., Jiang, C., Li, Y., Zhou, J., Wang, Y., Fu, G., Chen, Z. and Han, Z.
A novel gene expressed in the human hypothalamus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammali

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108369)

Schudy,A., Rump,A., Drescher,B., Koczan,D., Thiesen,H.-J.,
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                                                                                                                          gocotcottgattctgtggcccagcagggggctggctggctgcgcatgttg¢tgactt
GTCAGCAGCCTGCAGGGGAGGACTGCCGAGACTGT-TGCAGCGTCTTGGGGGTCAGCGCC
                                                                                   AF124523 108369 bp DNA PRI 24
Homo sapiens chromosome 8 clone Kox18-21 containing
protein 7 (2FP7) gene, complete sequence.
AF124523.1 GI:4325309
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			/evidence=not_experimental complement(1208112230) /note="GRAIL, score = 56.000% /evidence=not_experimental complement(1225512748) /rpt_family="LTR42" /evidence=not_experimental 1425514377 /note="GenScan, score = 10.27 /pp frame: 1 phase: 0" /evidence=not_experimental 1438614880		1581115858 /gene="zinc-finger protein 7 (2FP7)" /number=2 join(1585615858,1624616372,2334623462,2728529098) /gene="zinc-finger protein 7 (2FP7)" /note="mana acc.no. M29580" /codon_start=1 /product="zinc-finger protein 7" /protein_id="AAD17326.1" /db_xref="G1:4325310" /translation="MEVPTEGDVAVHFSREEWQCLDPGGRALYREVMLENHSSVAGLA /translation="MEVPTEGDVAVHFSREEWQCLDPGGRALYREVMLENHSSVAGLA GFLVFKPELISRLEGGEEPWVLDLQGAEGTEAPRTSKTDSTIRTENEQACEDMDILKS
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Merck-Rousseau, M.F. and Rosenthal, A. LE Direct Submission RNAL Submission Submitted (29. AAN-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Location/Qualifiers Source 1108369 (Organism-"Homo sapiens" /db_xref="taxon:9606" /chromosome="8" /chr		repeat_region 1377 .1734 /rpt_family="lama4"	exon /rpt_family="LlMA4" exon /avidence=not_experimental 2835. 2912 /evidence=not_experimental 2848. 2883 /ovidence=not_experimental 2848. 2883 /note="Xpound exon prediction, score = 77% (0%)" /evidence=not_experimental /rpt_family="Alusp" /rpt_family="Alusp" /evidence=not_experimental /evidence=not_experimental /rpt_family="Alusp" /evidence=not_experimental	repeat_region 33.636.5 repeat_region 33.636.5 /rpt_family="lulka" /rpt_family="lulka" /rpt_family="Likka" /rpt_family="Likka"	repeat_region 453

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PKCTECGKAFRLSSKLIGHQHIHTGERPYECEECGKAFGGSSLIHHQRIHTGERPY
GCRECGKAFSQOSOUVKHQFRHTGERPYECKECKAFSGSSTLAQHQRHHTGERPY
KASDSPSLVAHQRIHAVEKPFKCDECGKAFRWISRLSQHQLIHTGERPYTCKAF
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KKVNTIKKLHQCEDCEKIFRMRSHLIIHQRIHTGEKPYKCNDCGKAFNRSSRLTQHQK
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Pred. No. 2e-238;
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/rpt_family="LiME"
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Chudy, A., Schilhabel, M., Baumgart, C., Menzel, U., Weber, J., Schudy, A., Schilhabel, M., Baumgart, C., Menzel, U., Weber, J., Schudy, A., Schilhabel, M., Baumgart, C., Menzel, U., Weber, J., Direct Submission
Submitted (15-DEC-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany 1-75864: contig of 75864 bp; 75864-75865; gap of unknown size; 109039-117368: contig of 8330 bp; 117368-117369; gap of unknown size; 117369-128688: contig of 13374 pp; 1320 bp; 128688-128689:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36545 TGAGATGGTGCCAAAGTGCAGCTGACTCTTCCCACGACAGCCCTGCCCTTCCCATGAGGC 36486
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CCACCAGCCTGAAGCCTGACACCTTCAGGGACCAGCTCCAGGAGCTCTGCATCCCCCAAG 36906
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 8 clone BAC 704B241056 map
SEQUENCING IN PROGRESS ***, in unordered pieces.
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HTG; HTGS_PHASE1.
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8046. .9818
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/note="GRAIL"
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8005. .9818
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13949, .14111
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complement(12368. .12424)
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13354. 13491
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6689. .6747
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5627. .5906
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1078. .11384
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1519. .11638
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gap of unknown size; 128689-134145: contig of 5457 bp; 134145-134146: gap of unknown size; 134146-147620: contig of 13475-194146: gap of unknown size; 147621-149478: contig of 12620-147621-194078: contig of 2529 bp; 149479; gap of unknown size; 149479-151777: contig of 2529 bp; 15177-15178: gap of unknown size; 155131-157254: contig of 2124 bp; 155130-155130: gap of unknown size; 155131-157254: contig of 2124 bp; 157254-157255: gap of unknown size; 158492-174923: contig of 1238 bp; 157254-157255: gap of unknown size; 158493-174923: contig of 16431 bp;. contig of size of 157254-157255: gap of unknown size; 158493-174923: contig of size of 16431 bp;. contig of solution size; 158493-174923: contig of size of 16431 bp;. contig of solution size; 158493-174923: contig of size of 15431 bp;. contig of solution size of 15431 bp;. contiguence.
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5336..5612
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complement(750..820)
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1434..1555
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/chromosome="8"
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/note="MZEF"
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17389

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Enkaryota, Metazoan Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoan Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 128009)
S Rump, A., Rosenthal, A., Drescher, B., Weber, J., Schattevoy, R., Koczan, D., Thiesen, H.-J. and Merck-Rousseau, M.-F.

Experimental (OB-JAN-1299) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Location/Qualifiers

I. 128009
// Cranian="Homo sapiens"
// Ab_xref="#axon:9606"
// Chromosome="#a"
                                                                                                                                                                                                                                                                                                                                                                                                             AFI18808 128009 bp DNA PRI 30-JUN-1999
Homo saplens chromosome 8qter PAC clone P2G2, complete sequence.
AF118808
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                                                                                                                                                                                                                                                                                                                   17568 TGGCCCAGCAGCAGGGGGCCTGGCTGCCGCATGTTGCTGACTTTCGGTGGCGGGTGGATG 17509
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/clone="PAC clone P262"
/note="mapped to 8qter by FISH; identified by filter hybridization with 21nc finger specific probe: clone hybridization with 21nc finger specific probe: clone contains two sequencing gaps (60562-60589 and 68689-68687); orientation of the middle contig is not
                                                                                                 gactgcaggactgaccctcacttgaccagtcccattcagatccggcttggacaggcacc
                                                                                                                                                                                                                                                                                                      1076 aggetetteagtgagtgtttgaacgtaattatgtagttttetgtttaattgaaaagaga
                                                                                  agcttcagatgggtcagcataccgctttgaggtcccacaggccaagttccaggagctgc
                                                                                                                                       896 ggtacagcgtggccctggtcctaaaggagatggcagatctggagaagaggtgtgagcgca
                              tageaatetecaceagtgeeetggetegetecetgeageegagegteetgatgeagetga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acctggtcggggacttggccagcgtggtatttgggagccagcggcccctccttgattctg
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llarity 98.7%; Pred. No. 4.7e-238;
Conservative 0; Mismatches 13;
                                                                                                                                                                    16722. 16761
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16782. 16912
/rpt_family="L2a"
complement(17315. 17989)
/note="GRAIL"
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17351. 17527
/note="GRAIL"
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                                                                                                                                                                                                                                                                                              complement(17321. .17848)
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16383. .16634
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                                                                                    /rpt_family="L2"
16705. 16831
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of Molecular

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DD 126622 TGAGATGGTGCCAAAGTGCAGCTGACTGACTTCCCACGACAGCCCTGCCCTTCCCATGAGGC 126681
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Submitted (28-APR-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene for zinc
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e; Homo.
                                                                  /note="GenScan, score = 1186%, comment = Pl_377_aa
of owl|Pl5622|2F64_HUMAN ZINC FINGER PROTEIN CLONE
(FRAGMENT) - HOMO SAPIENS P = 1.2e-120 S = 1186"
                                                                                                                            tgagatggtgccaaagtgcagctgactcttcccacgacagccctggccttcccatcaggc
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8 PAC P5A4.00 containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Primates; Catarrhini; Hominidae;
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Rump,A., Schudy,A., Drescher,B., Kocz
Merck-Rousseau,M.-F. and Rosenthal,A.
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finger protein, complete sequence.
AF146367
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/organ1sm="Homo sapiens"
/db_xref="taxon:9606"
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5504. .6968
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/evidence=not_experimental
//A130. .47631
//Octe="Exon predicted by several exon prediction programs and by homology to GenBank entry AF024700_1: Homo sapiens clone B4-2 zinc finger protein mRNA, partial cds."
//evidence=not_experimental
                                                                                                                                                           programs
Kox9 mRNA
                                                                               programs
sapiens
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 exon prediction programs
HUMZIFIA_1: Homo sapiens

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complement(95143. 95187)
/note="Exon predicted by several exon prediction programs
and by homology to GenBank entry HSZNFPT7_1: H.sapiens
mRNA Acr Zinc-finger protein (ZNFpT7)."
/evidence=not_experimental
a 30514 c 28979 g 33352 t 47 others
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                                 2269. .2310
/note="Exon predicted by several exon prediction and by homology to GenBank entry HUMZNFN_1: Homo lon-binding protein (ZNF) gene, partial cds."
47097. 47263
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"Exon predicted by several
by homology to GenBank entry
finger protein mRNA, 3' end.
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Pred. No. 2.6e-237;
0; Mismatches 15;
                             /evidence=not_experimental 2269. .2310
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98.6%;
/note="Exon
and by homol
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                                                                                                                                                                                             tgtctgctgtggggggtgcaactccatacctgcatcatcctggtgatagtcacagtggcc
                                                                             79.5%; Score 1077.8; DB 40
llarity 98.4%; Pred. No. 1.4e-236;
Conservative 0; Mismatches 17;
bp frame: 1 phase: 2" /evidence=not_experimental 17500 a 18304 c 16802 g 16922
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Matches 1099;
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ORIGIN
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/note-"GenScan, score = 3534%, comment = P3_742_aa 44. .686
/note-"GenScan, score = 3534%, comment = P3_742_aa 44. .686
orl|Ply1097|ZNOT_HUMAN ZINC FINGER PROTEIN 7 (ZINC
FINGER PROTEIN KOX4) (ZINC P = 0.0 S = 3534"
/evidence-not_experimental
complement(44982. .46795)
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                                                                                                                                                        /gene="hypothetical"
/note="GenScan, score = -0.43%, comment = Initial_exon 108
bp frame: 1 phase: 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      comment - Internal_exon 134
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                                                                    /note="GenScan, score = 0%, comment = P2_471_aa GENSCAN predicted peptide is unknown ->NN (DEF2) prediction for sec struc composition: all beta sheet; overall class:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terminal_exon
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 /note="GenScan, score = 117.75%, comment
Single-exon_gene 1134 bp frame: 1 phase:
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36757. 37488
/gene="lypothetical"
/note="GenScan, score = 71.21%, cc/23 bp frame: 0 phase: 0"
/evidence=not_experimental
complement(44951. 60537)
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bp frame: 1 phase: 2.7
/evidence=not_experimental
complement(60537. 60658)
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bp frame: 2 phase: 2"
/evidence=not_experimental
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/note="GenScan, score = 0.77%,
bp frame: 2 phase: 0"
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                                                                                                                                                                                                                           /gene="hypothetical"
/note="GenScan, score = 0.51%,
bp frame: 0 phase: 2"
                                                                                                                                                                                                                                                                                                             /note="GenScan, score = 0.84%,
bp frame: 0 phase: 0"
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bp frame: 1 phase: 2"
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/evidence=not_experimental
complement(51365. .51454)
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                                 /evidence=not_experimental
                                                                                                                               'evidence-not_experimental
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/gene="hypothetical"
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Homo sapiens, clone RP11-18M17

Lupublished

E bases 1 to 133200)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collymore, A., Castle, A., Colangelo, M., Contes, P., DeArellano, K., Dowar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Howland, J. Garddyn, S., Grant, G., Raon, L., Ononelan, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Ofonenell, P., Mardun, J., Mardur, S., Kallin, J., McEnny, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Mortow, J., Naylor, J., Norman, C.H., O'Cooner, T., O'Domeell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Tirrell, A., Vasalilev, H., O'Connor, T., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Dec 10, 1999 this sequence version replaced gl:6056232.

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/Rw/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Research
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*** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133200)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L3701
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gap of unknown length
.1130: contig of 89 bp in length
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Homo sapiens clone RP11-18M17,
unordered pieces.
AC011951
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HTG; HTGS_PHASE1.
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/clone_lib="RPCI-11 Human Male BAC"
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Location/Qualifiers
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/organism="Homo sapiens"
//db_xref="taxon:9606"
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1 (bases 1 to 347);
S MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.
MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.
Direct Submission
CB10 1RQ, England: E-mail contact: humquery@sanger.ac.uk
E 2 (bases 1 to 347)
S Cross, S. H., Charlton, J. A., Nan, X. and Bird, A.P.
Purification of CpG islands using a methylated DNA binding columnat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                         884
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0; Mismatches 26;
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Best Local Similarity 83.9%;
Matches 146; Conservative C
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Matches 104; Conservative
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Direct Submission
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Submitted (21-JU-1997) Human Genetics Group, John Curtin School of Submitted (21-JU-1997) Human Genetics Group, John Curtin School of Subcra, ACT 0200, Australia
Canberra, ACT 0200, Australia
Location/Qualiflers
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Homo sapiens NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial
AF014882
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ITTTANTITLLNLYFYLLIYSTSTILLPWSNNVKWQFEHTKPPFLPTLIALTT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (Dases 1 to 104)
Wise,C.A., Sraml,M. and Easteal,S.
Departure from Neutrality at the Mitochondrial NADH dehydroger subunit 2 gene in Humans, but not in Chimpanzees
Genetics (1997) In press

[ (Dases 1 to 1041)
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100.0%; Pred. No. 9e-14;
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AF014883 1041 bp DNA PRI 06-MAY-1999
Homo sapiens NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial
gene encoding mitochondrial protein, partial cds.,
AF014883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Translation="MNPLAOPVIXSTIFAGTLITALSSHWFFTWVGLEMNMLAFIPVL
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ITPTINALTELNIYFYLRIYSTSITLLENGSNNVKKWQFEHTKPFLLPTLIALTT
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Homo sapiens NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial
gene encoding mitochondrial protein, partial cds.
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1 (bases 1 to 1041)
Wise, C.A., Srami, M. and Easteal, S.
Departure from Neutrality at the Mitochondrial NADH dehydrogenase Subunit 2 gene in Humans, but not in Chimpanzees

2 (bases 1 to 1041)
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Pred. No. 9e-14;
0; Mismatches 0;
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Direct Submission
Submitted (21-JUL-1997) Human Genetics Group, John curtin School of
Medical Research, The Australian National University, Mills Rd,
Canberra, ACT 0200, Australia
On Jul 2, 1998 this sequence version replaced 91:2582064.
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Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini: Hominidae: Homo.

1 (bases 1 to 1041)
Wise,C.A., Sraml,M. and Easteal,S.
Wise,C.A., Sraml,M. and Easteal,S.
Departure from Neutrality at the Mitochondrial NADH dehydrogenase subunit 2 gene in Humans, but not in Chimpanzees
Genetics (1997) In press
2 (bases 1 to 1041)
  at the Mitochondrial NADH dehydrogenase but not in Chimpanzees
Departure from Neutrality at the Mitochondrial NADH dehydrogena subunit 2 gene in Humans, but not in Chimpanzees Genetics (1997) In press 2 (bases 1 to 1041) Wise.C.A.
Direct Submission Submitted (21-JUL-1997) Human Genetics Group, John Curtin Schoo Medical Research, The Australian National University, Mills Rd, Canberra, ACT 0200, Australia
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Homo sapiens NADH dehydrogenase subunit 2 (ND2) ;
gene encoding mitochondrial protein, partial cds.
AF014886
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/organelle="mitochondrion"
/strain="Afr4"
/db_xref="taxon:9606"
/note="Bantu from Durban, South Africa"
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Homo sapiens NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial
gene encoding mitochondrial protein, partial cds.
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SIMAGSWGGLNQTQLRKILTASSITHMGWMAVLPYNPNMTILNLTIYILITAFLL
LNLNSSTTLLLSFWNKLFWLTPLLPSTLLSCGGLPPLTGFLFRNNSL
IPPTMATITLLNLYFYLRIYSTSTILLSCGGLPPLTGFLFRNNSL
IPPTMATITLLNLYFYLRIYSTSTILLSCGGLPPLTGFLFRNNSL
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Submitted (21-JUL-1997) Human Genetics Group, John Curtin School of
Medical Research, The Australian National University, Mills Rd,
Canberra, ACT 0200, Australia
On May 6, 1999 this sequence version replaced g1:3287312.
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Departure from Neutrality at the Mitochondrial NADH dehydrogenase subunit 2 gene in Humans, but not in Chimpanzees Genetics (1997) In press 2 (bases 1 to 1041)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1041)
Wise,C.A., Sraml,M. and Easteal,S.
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 9e-14;
tive 0; Mismatches 0; Indels 0
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/db_xref="taxon:9606"

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    /organism-"Homo sapiens"

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                                      GI:4755089
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TKKMNRSTEAAIKYFLTQATASMILLMAILFNNMLSGGWTWTNTTNQYSSLMIMMAM
AMKLGMAFHFWYPEVTGGTPFUSGLLLTWGKIAPISTMYOISPSLMYSLLLTLSIS
SIMAGSWGGANGGANGTPFTGSCLLLTWGKTAPISTNDWTILNITIYILLTRIST
LNLNSSTTTLLISRTWNKLTWITFLIFSTLLSLGGLPPLTGFLFRWNSI
IIPTIMATITILLNLYFYLRIYSTSITLLPWSNNVKWWGFEHTKPTPFLDTLTTTT
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Homo sapiens NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial
gene encoding mitochondrial protein, partial cds.
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Submitted (21-JUL-1997) Human Genetics Group, John Curtin School of
Medical Research, The Australian National University, Mills Rd,
Canberra, ACT 02000, Australia
On Jul 2, 1998 this sequence version replaced gi:2582068.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1041)
Wise,C.A., Sraml,M. and Easteal,S.
Departure from Neutrality at the Mitochondrial NADH dehydrogenase subunit 2 gene in Humans, but not in Chimpanzees
Genetics (1997) In press
2 (bases 1 to 1041)
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100.0%; Pred. No. 9e-14;
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/organelle="mitochondrion"
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TKKMNRRSTEAAIKYFLTQATASMILLMAILFNNMLSGGWTWTNTTNOYSSLAIMMAM
MKLGAAPHFWYPEVTGTPLTSGLLLTWGKLAPISINGYGISPLAUVSLLLTLSII
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LNLNSSTTTLLLSRTWNKLTWLTPLISSTLLGLGGLPPLTGFLFRKNNSI
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Direct Submission
Submitted (21-JUL-1997) Human Genetics Group, John Curtin School of
Medical Research, The Australian National University, Mills Rd,
Canberra, ACT 0200, Australia
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Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1041)
Wise,C.A., Sraml,M. and Easteal,S.
Departure from Neutrality at the Mitochondrial NADH dehydrogenase subunit 2 gene in Humans, but not in Chimpanzees

2 (bases 1 to 1041)
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Pred. No. 9e-14;
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/note="Bantu from Durban, South Africa"
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/transl_table=2
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                                                            /organelle="mitochondrion"
/strain="Afr5"
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TKKMNPRSTERAIKYELTOATASMILLMAILENNMLSGGWTWTSTTMOYSSLAIMMAM
AMKLGMAPFHFWVPEVTGGTPLTSGLLLLTWOKLAPISIMYQISPSLNVSLLLTLSIL
SIMACSWGGLNQTOLRKILAYSSITHHGWMAAVLPYNPNWTILNLTIYILTTAFLL
LINLNSSTTLLLGSTWNKLTWLTPLIPSTLLSKGLPPLTGFLPKWAIIEEFTKNNSL
LILPINSATTLLLNLYFYLRLYSTSITLLPWSNNVKWKWQFEHTKPTPFLPTLIALTT
LLLPISPSFMLML.
349 c 101 g 267 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="NADH dehydrogenase subunit 2"
/protein_id="Aac25448.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AF014889 1041 bp DNA PRI 06-MAY-1999
Homo sapiens NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial
gene encoding mitochondrial protein, partial cds.
AF014889 GI:3287317
SIMAGSWGGLNQTQLEKILAYSSITHWGWMAVLPYNDNYILNLTIYILTTTAFLL
LNLNSSTTTLLLSRTWNKLTWLTPLIPSTLESLGGLPPLTGFLPKWAIIEEFTKNNSL
IIPTIMATITLLNLYFYLRLIYSTSITLLPMSNNVKMKWQFEHTKPTPFLPTLALTT
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1 (bases 1 to 1041)

Wise,C.A., Sraml,M. and Easteal,S.
Departure from Neutrality at the Mitochondrial NADH dehydrogenase subunit 2 gene in Humans, but not in Chimpanzees

2 (bases 1 to 1041)

Wise,C.A.
Direct Submission
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                                                                                                                                                                                                  Gaps
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/organism="Homo sapiens"
/organelle="mitochondrion"
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Query Match

Search completed: May 15, 2000, 02:00:07 Job time: 11526 sec

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parathyroid;

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Sequence:

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Hypertension related calcium regulated gene - useful to develop products to treat or detect, e.g. hypertension, stroke, osteoporosis, heart failure, cancer, diabetes or asthma claim 2; pages 25-26; 46pp; English.

This nucleic acid sequence encodes the hypertension related calcium regulated gene (HoaRN), which was isolated from the rat parathyroid. Its expression is regulated by extracellular calcium concentration. An antibody against the protein, can be used to detect or modulate (e.g. enhance or inhibit) abnormal calcium levels. They can specifically be used to detect or reat, e.g. hypertension, hyperthyroidism, osteoporosis, heart failure, diabetes, stroke, cancer, inflammatory disease, and asthma.

Sequence 1100 BP; 260 A; 279 C; 315 G; 246 T;
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Rat Hypertension related calcium regulated gene (HCaRG) cDNA.
Hypertension related calcium regulated gene; HCaRG; rat parathyrc extracellular calcium concentration; antibody; hypertension; ss; hyperthyroidism; osteoporosis; heart failure; diabetes; stroke; cancer; inflammatory disease; asthma.
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Pred. No. 4.2e-114;
0; Mismatches 169;
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(TREW/) TREMBLAY J.
GOSSBATG F, Hamet P, Lewanczuk R, Tremblay J;
WPI: 98-07711/07.
P-PSDB; W37723.
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/note= "EF-hand like motif"
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             Q98748
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/product=
173. .196
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Matches 571; Conservative
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23-JUN-1997; CA0439.
21-JUN-1996; US-667495.
(GOSS/) GOSSARD F.
(HAME/) HAMET P.
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     GenCore version Copyright (c) 1993 - 2000
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01-JUN-1998 (first entry)
Human Hypertension related calcium regulated gene (HCaRG) cDNA.
Human Hypertension related calcium regulated gene; HCaRG; human parathyroid;
Hypertension related calcium regulated gene; HCaRG; human parathyroid;
extracellular calcium concentration; antibody; hypertension; ss;
hyperthyroidism; osteoporosis; heart failure; diabetes; stroke;
cancer; inflammatory disease; asthma.
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7 31-DEC-1997.
8 13-DEC-1997.
8 10-SEARD F.
9 10-SEARD F.
1 GOSSAIG F. Hamet P. Lewanczuk R. Tremblay J;
1 GOSSAIG F. Hamet P. Lewanczuk R. Tremblay J;
1 GOSSAIG F. Hamet P. Lewanczuk R. Tremblay J;
1 Hypertension related calcium regulated gene - useful to deving WPI: 99-07171/JO.
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1 Hypertension search and the sear
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This nucleic acid sequence encodes the hypertension related calcium regulated gene (HCaRG), which was isolated from the human parathyroid. Its expression is regulated by extracellular calcium concentration. The sequence display 75 percent homology to the rat form, with conserved areas such as the EF-hand like motifs and the initiating codon. An antibody against the protein, can be used to detect or modulate (e.g. enhance or inhibit) abnormal calcium levels. They can specifically be used to detect or treat, e.g. hypertension, hyperthyroidism, osteoporosis, heart failure, diabetes, stroke, cancer, inflammatory disease, and asthma.
Sequence 701 BP; 137 A; 204 C; 217 G; 139 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816
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                                                                                                                                                                          Indels 224;
                                                                                                                                                   Length 701
                                                                                                                                                    Score 338.8; DB 1;
Pred. No. 8e-80;
0; Mismatches 30;
                                                                                                                                                    25.0%;
llarity 72.2%;
Conservative
                                                                                                                                                                 Local Similarity
les 659; Conser
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standard; cDNA; 448 BP.
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A single-stranded DNA (or its complementary strand or the corresp.

Gouble-stranded DNA) which comprises one of the 7837 "GS" sequences

Given in T19001-T26837 and which is able to hybridise to part of

human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

Sequences were obtained from 3'-directed cDNA libraries prepared

sequences were obtained from 3'-directed cDNA libraries prepared

'c from various human tissues; synthesis of cDNA was initiated from the

'c and of mRNA by using poly(T) as the sole primer. Since the 3'-

call the 3'-oriented cDNA hybridise with Specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

C different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

c determined (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for

recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                995 gatccggcttggacaggcacctgagatggtgccaaagtgcagctgactttcccacgaca 1054
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Human gene signature HUMGS07932.
Gene signature: messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; Homo saplens.
W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3e-3
0; Mismatches
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97.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1995.
11-NOV-1994, J01916.
12-NOV-1993; JP-355504.
(MATZ) MATSUBARA K.
(CKUBY) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 97.8 Matches 177; Conservative
                                                                                         995 gatccggcttgga 1007
                                                                                                                     689 GATCCGGCTTGGA 701
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WPI; 95-206931/27.
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RESULT V86703

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The polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pltuitary, retina and colon cDNA libraries

E.g. human blood, kidney, foetal lung, placenta, testes, brain,

E.g. human blood, kidney, foetal lung, placente,

Claim 1; Page 321; 633pp; English.

Claim 1; Page 321; 633pp; English.

C. This sequence represents an expressed sequence tag (EST), and is a comply considered of the invention. The polynucleotides of the invention are all secreted EST sequences and proteins encoded by them are predicted to sources. The EST sequences and proteins encoded by them are predicted to have useful blological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities

C. freating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activity, chemotactic/chemokinentic activity, activity, chemotactic/chemokinentic activity, chemotactic/chemokinentic activity, activity, chemotactic/chemokinentic activity, chemotactic/chemokinentic activity, tumour inhibition activity, the EST sequences are also stated to be useful for gene
                                                  Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Addressin cell adhesion molecules - used to develop products for detection of inflammatory conditions or cancer and for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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Human mucosal adressin cell adhesion molecule-1 gene exon 3.

Mucosal addressin cell adhesion molecule-1; MAGCAM-1; human;

Cancer; tumour; inflammation; transplant rejection; arthritis;

rheumatoid arthritis; infection; inflammatory bowel disease;

autoimmune disease; experimental autoimmune encephalitis;

dermatosis; diagnosis; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                     Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; WPI; 99-070076/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 attacccacataggatgaataatagcagttctaccgtacaaccccg 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 G;
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Pred. No. 2.4e-18;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 C;
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01-NOV-1996; WO-U17549.
(HUMA-) HUMAN GENOME SCI INC.
(UYMA-) UNIV AUCKLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.78;
99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V38226 standard; DNA; 350 BP.
                                                                                                                                                                                                                       15-OCT-1998.
10-APR-1998; U06954.
10-APR-1997; US-835913.
(GEMY) GENETICS INST INC.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 BP;
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Addressin cell ad
                             EST clone BG461
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WO9820110-A1.
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preventing inflammatory conditions

Claim 1; Page 114: 164pp; English.

This nucleic acid molecule comprises exon 3 of the novel human rules acid molecule comprises exon 3 of the novel human mucosal tascular addressin cell adhesion molecule MAGCAM-1 gene that maps to chromosome 19, band pl3.3. A MAGCAM-1 genomic clone that maps to chromosome 19, band pl3.3. A MAGCAM-1 genomic clone that maps to chromosome 19, band pl3.3. A MAGCAM-1 free form a cosmid library by screening with a human EST homologue of murine MAGCAM-1. The 5, untranslated region and exons 1-5 (see V38223-28), in various comprise the coding regions of MAGCAM-1(a) and its splice variants MAGCAM-1(b-e) (see V38210-05). Exons 2 and 3 encode the N-terminal immunoglobulin-like domains. The invention provided are diagnostic methods for detecting cancer or a provided are diagnostic methods for detecting cancer or a rithritis, rheumatory condition (e.g. transplant rejection, cernatosis, inflammatory conditions arthritis, infection detecting cancer or a rithritis, rheumatoid arthritis, infection, demandosis, inflammatory concephalitis), and therapeutic methods for treating an individual compounds for relates to a method of screening compounds for the invention also relates to a method of screening compounds for the oblity to regulate expression of MAGCAM-1(a-e) from its promoter.

Sequence 350 BP: 52 A; 129 C; 120 G; 49 T;
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13-1011997 (first entry)
Leishmania tropica Lt-210 antigen cDNA.
Leishmaniasis; vaccine; diagnosis; Lt-210; antigen; immunogen; ss.
Leishmania tropica strain MHOM/SA/91/WR1063C.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GAGGAGGAGGAGCCCCCAGGGGGACGAGGACGTGCTGTTCAGGGTGACAGAGCGCTGG
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A genomic DNA molecule (16218) encodes a 210 kDa immunogenic Leishmania tropica antigen (W11217), designated Lt-210. It was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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Best Local Similarity 47.2
Matches 137; Conservative
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20-SEP-1996; U15185.
22-SEP-1995; US-533669.
(CORI-) CORIXA CORP.
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WPI: 97-202888/18.
P-PSDB; W11217.
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obtd. by screening a L. tropica promastigote expression library with sera isolated from viscerotropic leishmaniasis patients. DNA molecules (see also T62135-37, T62139) encoding Leishmania entigens can be incorporated into vectors and used to produce recombinant antigens, or immunogenic portions of them, in host cells for use in vaccines against Leishmaniasis, or may themselves be used as sections for in vivo immunogen generation.

Sequence 1771 BP: 279 A; 552 C; 672 G; 268 T;
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Leishmania antigen Lt-210 coding sequence.
Leishmania antigen; immune response; infection detection; therapy;
humoral response induction; cellular response induction; cancer;
interleukin-12 production; ss.
                                                                                                                                                                                                                                                                                                                                           1050 ccgcgcccrcgaragcagrcgccrrrgcacrccrcgcrgragcrcgacgrcgcggccg
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Campos-Neto A, Dillon DC, Reed SG, Skeiky YA, Webb JR;
WPI; 98-447242/38.
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/product= Lt-210
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V47558, V47558
LD V47558 standard; DNA; 1771
AC V47558;
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27-AUG-1997; US-920609.
12-FEB-1997; US-798841.
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and/or cellular response, specifically of Th1 type, particularly including induction of interleukin-12 (IL-12) production. They may thus be used more generally to treat any condition (e.g. bacterial, viral or protozoal infection, or cancer) which responds to IL-12. Sequence 1771 BP; 279 A; 552 C; 672 G; 268 T;
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                                                                                                                                                                                                                                              930 GGCCTGGGAGCGGCCTGCTCGTGCATGGCCTCCAGGCGGGCCGCCTCCTCGAG 871
                                                                                                                                                                                                                                                                                          870 GGCCTGGACACGGGCCTGCTCGCCCTCGTGACATCCAGGCGGGCCGCCTCCTCGGC 811
                                                                                                                                                                                                                                                                                                                                          810 GCCTCCAGCTCCGCGCGCGCAGACGCGTGCCTCGAGGGCCTGGACGCGGGCCTGCTC 751
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Addressin cell adhesion molecules - used to develop products for detection of inflammatory conditions or cancer and for treating orceventing inflammatory conditions.

Claim 2; Page 88-90; 164pp; English.

This nucleic acid molecule, designated clone HEBBC23 and deposited as ATCC 97759, codes for human mucosal vascular addressin cell adhesion molecule MAACAM-1(a) (see W60607), a novel cell surface
                                                                                                                                                                                                                         gtgcagcgtcttggggtcagcgccaacctgccggaggagcagctgggtgccttgctggca
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28-SEP-1998 (first entry)
Human mucosal adressin cell adhesion molecule-1(a) DNA.
Mucosal addressin cell adhesion molecule-1; MAdCAM-1(a); human;
cancer; tumour; inflammation; transplant rejection; arthritis;
rheumatoid arthritis; infection; inflammatory bowel disease;
autoimmune disease; experimental autoimmune encephalitis;
dermatosis; diagnosis; therapy; ds.
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                                                                                3.2%; Score 44; DB 1; Length 1771;
45.8%; Pred. No. 0.031;
Live 0; Mismatches 180; Indels
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P-PSDB; W60607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 V38201 standard; DNA; 1536 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 45.8
nes 152; Conservative
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                                                                                            Best Local Sim
Matches 152;
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adhesion molecule that shows homology to murine MAGCAM-1. The designated MAGCAM-1(a) as well as 4 splice variants, designated MAGCAM-1(b), -1(c), -1(d) and -1(e) (see V38201-05).

These 5 nucleic acid molecules were discovered in a cDNA library farious from human foctal brain cells following a database search for human ESTS maving homology for mouse MAGCAM-1. The genes were also identified in cDNA libraries from the small intestine, colon, spleen and pancreas. The invention also provides MAGCAM-1(a-e) proteins (see W60607-11)/M vectors, host cells, recombinant methods of proteins (see W60607-11)/M vectors, host cells, recombinant methods of proteins (see W60607-11)/M vectors, host cells, recombinant methods of producing the polypeptides, as well as methods for detecting cancer or a pathological inflammatory condition, and thermpettic methods for treatting an individual in need of a capacity of fany of MAGCAM-1(a-e). Genomic DNA molecules comprising the 5' untranslated region and exons 1-5 (see V8223-28) which, in various combinations, comprise the coding of any of the MAGCAM-1 police variants are also claimed. The novel human MAGCAM-1 polypeptides can be used as a target for the diagnosis and treatment of inflammation conditions such as transplant rejection, arthritis, rheumatoid arthritis, infection, dermatosis, inflammatory bowel disease, and autoimmune encephalitis. Sequence 1536 BP; 263 A; 571 C; 442 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 ggcccagcttcctccagaggtggcagcaatggcccggctactaggggacctagacaggag 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 GICCCIGGIGACCCGGAGGIGGCCIGIACGGCCCACAAAGICACGCCCGIGGACCCCAA 434
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28-SEP-1998 (first entry)
28-SEP-1998 (first entry)
Mucosal adressin cell adhesion molecule-1(b) DNA,
Mucosal addressin cell adhesion molecule-1; MAdCAM-1(b); human;
cancer; tumour; inflammathon; transplant rejection; arthritis;
rheumatoid arthritis; infection; inflammatory bowel disease;
autoimmune disease; experimental autoimmune encephalitis;
dermatosis; diagnosis; therapy; ds.
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Pred. No. 0.11;
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1459. .1464
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52. .1098
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Matches 136; Conservative
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/*tag= a
1. .49
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Key
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                                                                                                                                               preventing inflammatory conditions or cancer and for treating or preventing inflammatory conditions

Sclaim 2: Page 92-94; Id4pp; English.

Calm 2: Page 92-94; Id4pp; English.

Chann 2: Page 92-94; Ed4pp; English.

Cc This nucleic acid molecule, designated clone HSKCW36, codes for human mucosal vascular addressin cell adhesion molecule MAdCAM-I(b) (see W860608), a novel cell surface adhesion molecule that shows composed to mucrime MAdCAM-I. The invention relates to human mucosal vascular as well as 4 splice variants, designated MAdCAM-I(b), and -1(e) see V38201-05). These 5 nucleic acid molecules were discovered in a CDNA library derived from human clocatel brain cells following a database search for human ESTS (compless were discovered in a CDNA library derived from human crocated brain cells following a database search for human ESTS (composed MadCAM-I). The genes were also identified in CDNA libraries from the small intestine, colon, spleen and composed in cDNA libraries from the small intestine, colon, spleen and carried propertides, as well as methods for identifying agonists and carried propertides, as well as methods for identifying agonists and carried propertides, as well as methods for detecting cancer or a pathological inflammatory condition, and therapeutic methods for treating an individual in need of a reduction in activity of any of the MAGCAM-I polypeptides can be comprise the coding region of any of the MAGCAM-I splipeptides can be conditions such as transplant rejection, arthritis, rheumatoid autoimmune disease, including chronic relapsing experimental autoimmune encephalities.

Sequence 1488 BP; 255 A; 543 C; 435 G; 255 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 ccagaggtggcagcaatggcccggctactaggggacctagacaggagcacgttcagaaag 444
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                                                                                                                         Addressin cell adhesion molecules – used to develop products for detection of inflammatory conditions or cancer and for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 GAGGAGGAGGAGGACCCCCAGGGGGACGAGGACGTGCTGTTCAGGGTGACAGAGCGCTGG
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Human mucosal addressin cell adhesion molecule-1 cDNA clone 20.
Mucosal addressin cell adhesion molecule-1: MAGCAM; antibody;
leukocyte infiltration; ulcerative colitis; Crohn's disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 41.6; DB 1; Length 1488; 46.8%; Pred. No. 0.12; tive 0; Mismatches 149; Indels 0
                                                                     Greene JM, Krissansen GW, Leung EYF, Ni J, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   628 CTGCCTGGCTTGGAGCTCAGCCACCGCCAGGCCATCCCCG 667
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01-NOV-1996; U17549.
01-NOV-1996; WO-U17549.
(HUMA-) HUMAN GENOME SCI INC.
(UXAU-) UNIV AUCKLAND.
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Best Local Similarity 46.8
Matches 131; Conservative
                                                                                          98-286926/25.
                                                                                                        P-PSDB; W60608
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385 ccagaggtggcagcaatggcccggctactaggggacctagacaggagcacgttcagaaag 444
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CDNA clone 20 (T39751) codes for human mucosal addressin cell
adhesion molecule-1 (MAdCAM-1) (W05322), whose cellular adhesion
molecule-1 (MAdCAM-1) (W05322), whose cellular adhesion
function is alpha4beta7 integrin-dependent and pref. is selective
for alpha4beta7. It was fisolated from a CDNA library prepd. from
mesenteric lymph nodes (MLN) of a patient with group's dagase,
using a macaque MAdCAM-1 CDNA clone (T39752) as probe. Another
clone (T39750), encoding a different human MAdCAM isoform (W05321),
was isolated from a histologically normal MLN library. MAdCAM
nucleic acids can be used fis probes to detect polymorphic or
allelic variants of MAGCAM, or used to produce recombinant MAMCAM
in host cells.
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0; Mismatches 149; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ringler DJ;
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Location/Qualifiers
1. .1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X35280 standard; DNA; 1539
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Matches 131; Conservative
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01-SEP-1995; US-523004.
(LEUK-) LEUKOSITE INC.
BLISKIN MJ, Newman W, E
WPI: 96-384445/38.
P-PSDB; W05322.
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1. .54
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L2-FEB-1996; U02153
                                                                                                                                                                                        signal_peptide
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X35280
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New polypeptide(s) for inhibiting MadcAM-1-mediated interactions - useful for treatment of diseases associated with leukocyte

The special for treatment of diseases associated with leukocyte

Infiltration of tissues, especially inflammatory bowel disease and

Insular-dependent diabetes mellitus

CC fles specification describes inhibitors of mucosal addressing cell

adhesion molecule-1 (MAdcAM-1) mediated interactions. These inhibitors

CC madcam, and which have groups bonded to the N and C terminals.

CC madcan, and which have groups bonded to the N and C terminals.

CC with leukocyte infiltration of tissues expressing the MAdcAM-1,

CC with leukocyte infiltration of tissues expressing the MAdcAM-1,

mellitus. Inflammatory bowel disease and insulin-dependent diabetes

CC with leukocyte infiltration of tissues expressing the MAdcAM-1,

mellitus. Inflammatory bowel disease and insulin-dependent diabetes

CC specially inflammatory bowel disease, ilettis, coeliac disease,

contropathies, microscopic or collagenous collitis, coeliac disease,

arthropathies, microscopic or collagenous collitis, coeliac disease,

cc flecama nasstonosis: The inhibitors can also be used to inhibit the

conding of a cell expressing a ligand for MadcAM-1 or the cell surface to

comparison of antibodies which selectively bind MadCAM-1. These antibodies

cc gastroenteritis or inturn be used to identify cells expressing MadcAM-1. They are also useful in diagnostic and research applications,

confirmation of antibodies which selectively bind MadcAM-1. They are also useful in asmple. The compounds can also be

cut turn be used to identify cells expressing MadcAM-1 on their cell

can in turn be used to identify cells expressing madcam-1 cell

can in turn be used to identify cells expressing madcam-1 cell

can in turn be used to identify cells expressing the comparities of expression of this expressing madcam-1 cells

collabelled and used to detect alpha-bert expressing the companity and the cell expressing the controper cells expressing the com
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Human mucosal addressin cell adhesion molecule-1 cDNA clone 4.
Mucosal addressin cell adhesion molecule-1; MAdCAM; antibody;
leukocyte infiltration; ulcerative colitis; Crohn's disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression of this the surface of cells. The present sequence encodes human MAGCAM-1. Sequence 1539 BP; 268 A; 570 C; 442 G; 259 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    628 CIGCCIGGCIIGAGCICAGCCACCGCCAGGCCAICCCG 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1%; Score 41.6; DB 46.8%; Pred. No. 0.13;
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                                    17-JUL-1997, U00291.
03-JAN-1996; US-582740.
(LEUK-) LEUKOSITE INC.
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Best Local Similarity 46.8
Matches 131; Conservative
                                                                                                                                                                                            P-PSDB; Y02069
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385 ccagaggtggcagcaatggcccggctactaggggacctagacaggagcacgttcagaaag 444
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CDNA clone 4 (T39750) codes for human mucosal addressin cell
adhesion molecule-1 (MadCAM-1) (W05212), whose cellular adhesion
function is alpha4beta7 integrin-dependent and pref. is selective
for alpha4beta7. It was isolated from a cDNA library prepd. from
normal human mesenteric lymph nodes (MLN) using a macaque MAdCAM-1
cDNA clone (T39752) as probe. Another clone (T39751), encoding
a different human MAdCAM isoform (W05322), was isolated from the
MLN of a partient with Crohn's disease. MAdCAM nucleic acids can
be used as probes to detect polymorphic or allelic variants of
MAdCAM, or used to produce recombinant MAGCAMs in host cells.
Sequence 1624 Bp; 295 A; 610 C; 454 G; 265 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1999 (first entry)
CDNA encoding human MAGCAM-1.
Mucosal addressing call addressing callibration; disease; inflammatory bowel disease; ulcarative collits; Crohn's disease; ileitis' coeliac disease; nontropical Sprue; enteropathy; seronegative arthropathy; collits; essinophilic gastroenteritis; pouchitis; proctocolectomy;
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                                                                                                                                                                                                                                                                                              12-FEB-1995; UC2153.
10-FEB-1995; US-2380857.
10-FEB-1995; US-233004.
10-SEP-1995; US-233004.
LEUK-) LEUKOSITE INC.
Briskin MJ. Newman W. Picarella D, Ringler DJ;
WPI; 90-384445/38.
P-PSDB; W05321.
Nucleic acid encoding primate mucosal addressin cell adhesion molecule-1 - and antibodies against this protein, useful to trea diseases associated with leukocyte infiltration e.g. ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41.6; DB 1; Length 1
Pred. No. 0.13;
0; Mismatches 149; Indels
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           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.18;
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Disclosure: Fig 4: 108pp; English.

The specification describes inhibitors of mucosal addressing cell

adhesion molecule-1 (MadGAM-1) mediated interactions. These inhibitors

adhesion molecule-1 (MadGAM-1) mediated anino acid motif LDTs of

comprise peptides which mimic the conserved amino acid motif LDTs of

ANAGAM-1, and which have groups bonded to the N and C terminals.

ANAGAM-1, and which have groups bonded to the N and C terminals.

CC minitures can be used for the treatment of a disease associated

with leukocyte infiltration of fissues expressing the MAdGAM-1,

cspecially inflammatory bowel disease and insulin-dependent diabetes

construction of infiltration of tissues expressing the MAdGAM-1,

construction of infiltration and insulin-dependent diabetes

confirmed infiltration of fissues expressing with seronegative

confirmed infiltration of an antibodies on the collagenous collitis, coelinc disease,

confirmed of a cell expressing a ligand for MAGCAM-1 on the cell surface to bonding of a cell expressing indiagnostic and research applications,

confirmed and used to identify cells expressing MAGCAM-1. These antibodies

confirmed in turn be used to identify cells expressing MAGCAM-1 on their cell

confirmed of this the surface of cells. The present sequence

confirmed of this the surface of cells. The present sequence

confirmed broad of this the surface of cells. The present sequence
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HTLAR33 encoding cDNA (EST derived sequence).
YAK-1; serine-threonine protein kinase; HTLAR33; bone loss; ARDS;
Infilamatory disorder: osteoporosis; Adult Respiratory Disease Syndrome; arthritis; psoriasis; dermattits; asthma; allergy; infection; HIV-1; arthritis; psoriasis; dermattits; asthma; allergy; infection; HIV-1; HIV-2; cachexia; immunodeficient disorder; septic shock; pain; injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 ttgctgaagtttgtggtcagcagcctgcagggggaggactgccgagacggtgtgcagcgt 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                        useful for treatment of diseases associated with leukocyte infiltration of tissues, especially inflammatory bowel disease and insulin-dependent diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448 recerecreseseseceassaacresasseseseseaaseceresseseseseseas
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                                                                                                                                                                                                                                                                           New polypeptide(s) for inhibiting MAGCAM-1-mediated interactions - useful for treatment of diseases associated with leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 41.6; DB 1; Length 19
46.8%; Pred. No. 0.13;
tive 0; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625 gaccagetecaggagetetgeatececeaagaeetggteg 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X17775 standard; cDNA; 1338 BP.
X17775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 131; Conservative
                                                                                                                                         (LEUK-) LEUKOSITE INC.
Schwender CF, Shroff HN:
API: 97-384978/35.
                                                                                                 US-582740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                    03-JAN-1997; U00291
04-JAN-1996; US-582
                                                                                                                                                                                                                                                               P-PSDB; Y02068
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P-PSDB; W49498.

PT 9019ucleotides - useful as diagnostic reagents and for prevention polyuucleotides - useful as diagnostic reagents and for prevention polyuucleotides - useful as diagnostic reagents and for prevention and canner. HIV infections and angina pectoris

PT and canner, HIV infections and angina pectoris

PT and canner, HIV infections and angina pectoris

PS claim 13; Page 15-17; 30Pp; English.

CC comprising the HTLARR3 nucleic acid are used for the recombinant comprising the HTLARR3 nucleic acid are used for the recombinant comprising the HTLARR3 nucleic acid are used for the recombinant comprising the HTLARR3 nucleic acid are used for the recombinant comprising the HTLARR3 nucleic acid are used for the recombinant comprising the HTLARR3 nucleic acid are used for the recently for antagonists. These can be used in treatment to screening for antagonists, agonists. These can be used in treatment to comprise or treated includes now lose and inflammatory disorders including osteoporosis, Adult Respiratory Disease Syndrome (ARDS), Rheumatorid arthritis, astham, allergies; bacterial, fungal, protezoan and viral infections, especially those caused by HIV-1 or protezoan and viral infections, especially those caused by HIV-1 or protezoan and viral infections, especially those caused by HIV-1 or protezoan and viral infury; cancers; anorexia; building prostatic hypertension; septic shock; pain; injury; cancers; anorexia; building prostatic hypertension; curliary retention; angina pectoris; ulcers; benign prostatic hypertension; and psychotic and neurological disorders, including schizophrenia, and psychotic and psychotic and neurological disorders; benign prostatic hypertension; anticers; and psychotic and neurological disorders; benign prostatic hypertension; anticers and psychotic and disorders including schizophrenia, and psychotic and as Huntington's disease or Gilles de la Tourette's and system. TLAR33 polypeptides are also useful for mapping genes to chromosomes, allowing gene inheritance to be studied 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1999 (first entry)
YAR-1 related serine/threonine protein kinase-HTLAR33 encoding cDNA.
YAR-1; serine-threonine protein kinase; HTLAR33; bone loss; ARD5;
YAR-1; serine-threonine protein kinase; HTLAR33; bone loss; ARD5;
Inflammatory disorder; oswpoporosis; Adult Respiratory Disease Syndrome;
arthritis; psoriasis; dermatitis; asthma; allergy; infection; HIV-1;
arthritis; psoriasis; dermatitis; asthma; allergy; infection; HIV-1;
cachexia; immunodeficatent disorder; septic shock; pain; injury;
cancer; anorexia; bulimia; Parkinson's disease; cardiovascular disease;
neurological disorder; Huntington's disease; gene therapy; gene mapping;
                            therapy; gene mapping;
cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coggaggagcagctgggtgcctgctggcaggcatgcacacactgctccagcaggcctc 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
          anorexia; bulimia; Parkinson's disease; Ca
ical disorder; Huntington's disease; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.0%; Score 40.2; DB
53.5%; Pred. No. 0.28;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 C;
                               neurological disorder; Huntington's d
Gilles de la Tourette's syndrome; ss.
                                                                                                                                                      21-UUL-1998; 305794.
20-FEB-1998; US-027064.
28-UUL-1997; US-053924.
(SMIK ) SMITHKLINE BEECHAM CORP.
BEISSME DJ, SNADON U;
WPI; 99-108353/10.
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                                                                                                                                      03-FEB-1999.
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Best Local S:
Matches 84;
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KW Gilles de la Tourette's syndrome; ss.

By Garbal.

By 6363-Al.

By 7364-Al.

By 736-Al.

By 7377-Al.

By 737-Al.

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Search completed: May 15, 2000, 01:46:13 Job time: 9837 sec 3

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Sequence 1, Al
Sequence 11, Al
Sequence 2, Al
Sequence 7, Al
Sequence 1, Al
Sequence 3, Al
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                                       Sequence 6, A Sequence 1, A Sequence 18, A Sequence 4, A Sequence 5, A Sequence 5, A Sequence 3, A Sequence 3, A
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                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08533669A

Sequence 7, Application US/08533669A

Setting No. 5834992

GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Washington
COUNTRY: USA

ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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3.2%; Score 44; DB 3; Length 1771;
Best Local Similarity 45.8%; Pred. No. 0.0099;
Matches 152; Conservative 0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-849-389-6
US-08-20-747-1
US-08-20-747-1
US-08-50-76-4
US-08-550-76-5
US-08-650-76-5
US-08-650-76-3
US-08-650-76-1
US-08-650-76-1
US-08-650-76-1
US-08-68-11-1
US-08-284-46-2
US-08-284-46-7
                      60-075A-17
                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                    2793
2793
12412
1895
1171
1171
1171
1208
12001
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1426
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY;
; LOCATION:
US-08-533-669A-7
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                                                                                                       May 15, 2000, 01:50:08 ; Search time 76.12 Seconds (without alignments) 2260.217 Million cell updates/sec
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Patent No. 52
Patent No. 52
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Sequence 2
Sequence 3
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1: /cgn2_6/ptodatu/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodatu/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodatu/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodatu/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodatu/2/ina/5C_COMB.seq:*
6: /cgn2_6/ptodatu/2/ina/FOCMB.seq:*
7: /cgn2_6/ptodatu/2/ina/PcrtrS_COMB.seq:*
7: /cgn2_6/ptodatu/2/ina/PcrtrS_COMB.seq:*
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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US-08-728-323A-1
US-08-76-577-1
PCT-US96-00005-1
US-08-396-650-2
US-08-396-650-3
US-08-396-650-3
US-08-396-650-3
US-08-396-650-4
US-08-768-626-4
US-08-768-626-4
US-08-768-626-4
US-08-768-625-4
US-08-642-255-48
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US-08-465-500-31
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US-08-642-255-50
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                                                                                                                                                                                                                                                                                                            226296 seqs, 63486255 residues
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    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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1355
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Match Length DB
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Maximum DB seq length: 1000000
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Perfect score:
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Best Local Similarity
``hea 75; Conserva
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5212296-16
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                                                                                                                                                                                          ggcatgcacacactgctccagcaggccctccgtctgccccccaccagcctgaagcctgac 615
                                                                                                                                                                                                                  810 ceccrecaerceceesasaceceracicercercassesceresaceces
                                      436 ttcagaaagttgctgaagtttgtggtcagcagcctgcaggggggaggactgccgagacggt 495
                                                                           990 CTCATCTTTTCCTCCTCCTCAGCCTCCAGCTCCGCGCAGAGACGCGCTGCCTCCTCGAG 931
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Score 44; DB 4; Length 1771;
Pred. No. 0.0099;
0; Mismatches 180; Indels
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Patent No. 5965142
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Dead, Steven G.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: DELECTION OF L. tropica INFECTION NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPPRATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 04-AUG-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5: SEED and BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICALLOW ... 04-AUG-1995
CLASSIFICATION: 424
ATTORNEY'AGENT INFORMATION:
NAME: No. 5965142tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 210121.405
TELEPHONE: (206) 622-4900:
TELEFAN: (206) 682-6031
TELEFAN: 3723836 SEEDANDERRY
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1771 base pairs
LENGTH: 1771 base pairs
                                                                                                                                                                                                                                                                                                                                                676 agcgtggtatttgggagccagcggccctcct 707
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Best Local Similarity 45.8%;
Matches 152; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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94104-7092
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; LOCATION:
US-08-511-872-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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US-08-511-872-1/c
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574 cagcaggecetecgtetgececeaceageetgaageetgacacetteagggaceagete 633
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1050 ccececcresarascastrescerrirscacretescretascresastresces
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Patent No. 5212296
Papelicant: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
TEPPERMAN, JAMES M.
TILLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
5212296-5
FALCANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNE; J. O'KEERE, DANIEL, P.; OWERE, A.; FOMES, A.; TEPPERMAN, JAMES, A.; TEPPERMAN, TEPPERMAN, JAMES, A.; TEPPERMAN, TEPPERMAN, JAMES, A.; TEPPERMA
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56.0%; Pred. No. 0.13;
tive 0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
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907 IGANTEGECCCCCAGCICCGCCGACACCICCACCGCCCICIGCAGCAGCAGTAGCGCGCIC 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
TITLE OF INVENTION: D29 SHUTILE PHASMIDS AND USES THEREOF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  687 tgggagccagcggcccttcttgattctgtggcccagcagc 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.8%; Score 38.6; DB 1; 1
Best Local Similarity 48.4%; Pred. No. 0.48;
Matches 107; Conservative 0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN CITY: NEW YORK STATE: NEW YORK STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10016 COMPUTER READBLE FORM: MEDIUM TYPE: 3.5 INCH 1.44 MD STORAGE MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/614,770A
FILING DATE: MARCH 7, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/402
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: (212) 597-5995
TELETAX: (212) 286-0854 or 286-082
TELETAX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08614770A; Patent No. 5773267
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EDNESS: DOUBLE
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ORIGINAL SOURCE:
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                                                          ; LOCATION:
US-08-242-677-1
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US-08-614-770A-1
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APPLICANT: Way Foon W. Fo
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:

NAME: Mayfield, Danise L.

REFERENCE/DOCKET NUMBER: UTSD:401

TELECOMMONICATION:

TELEPHONE: 713-787-1400

TELEFAX: 713-789-2679

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5173 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.6; DB 7;
Pred. No. 0.16;
0; Mismatches 59;
                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-A0C-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 2.9%;
Best Local Similarity 56.0%;
Matches 75; Conservative
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NUMBER OF SEQUENCES: 19
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5212296-5
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US-08-242-677-1/c
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DB 2; Length 49272;
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Busso, James J.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Moore, Patrick S.
APPLICANT: Raposition Raposition From Raposit's TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43254 ATCATGGTTGCCCAGGATCAGCCGCTTGCGGCCTGGCCGGTTCA 43297
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CLASSIFICATION: 435
NATORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/POCKEY NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEDHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
        Score 38.4; DB 2;
Pred. No. 1.6;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08728323A Patent No. 5948676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
             2.8%;
                                                     Best Local Similarity 48.2
Matches 108; Conservative
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-728-323A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 11
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US-08-728-323A-1
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                      Query Match
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Length 3489;

DB 4;

2.8%; Score 37.8;

Query Match

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                                                       497 tgcagcgtcttggggtcagccaacctgccggaggagcagctgggtgccctgctggcag 556
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DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                        617 cetteagggaceagetecaggagetetgeatececeaagacetggtegggaettggeea
                                                                                                                                           557 gcatgcacacactgctccagcaggccctccgtctgccccccaccagcctgaagcctgaca
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                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.8; DB 3;
Pred. No. 1.9;
0; Mismatches 132;
Pred. No. 0.65;
0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ghang, Yuan APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Releasen, Isladore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: HERPESVIRUS, DN.
TITLE OF INVENTION: HERPESVIRUS, DN.
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08770379
Patent No. 5849564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CARACTERISTICS:
LENGTH: 32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.0%;
Matches 117; Conservative
    47.08;
    Best Local Similarity 47.0
Matches 117; Conservative
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MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
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US-08-770-379-20
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FEATURE
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                     497 tgcagcgtcttggggtcagcgccaacctgccggaggagcagctggtgccctgctggcag 556
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                                                                     gcatgcacacactgctccagcaggccctccgtctgcccccaccagcctgaagcctgaca
                                                                                                                                            617 cettcagggaccagetccaggagetctgcatececcaagacetggtegggaettggeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION ERRORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin r. 205/m3. DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,577
FILING DATE: 12-DEC-1994
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Banner, Birch, McKie & Beckett
1001 G Street N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,141

FREFERENCE/DOCKET NUMBER: 01107.48554

TELECOMMUNICATION INFORMATION:
TELEPRAX: 202-508-910

TELEFAX: 202-508-929
TELERX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3443 Base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1001 G Street N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5728523
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                           737 ggctgccgc 745
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US-08-366-577-1
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US-08-366-577-1
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                                                                                           490 gacggtgtgcagcgtcttggggtcagcgccaacctgccggaggagcagctggggtgcctg 549
                                                                                                                                                                                                                                                                                                                                                                            610 cctgacaccttcagggaccagctccaggagctctgcatcccccaagacctggtcggggac 669
                                                                                                                                                                                                                                                                                 550 ctggcaggcatgcacacactgctccagcaggccctccgtctgccccccaccagcctgaag
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APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMNS WITH REPLICATION ERRORS
NUMBER OF SOUGNCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
         Length 3435;
  Score 37.4; DB 2; Length 3. Pred. No. 0.83; 0; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATONNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
TELECOMMUNICATION NUMBER:
TELECOMMUNICATION NUMBER:
TELECOMMUNICATION NUMBER:
TELECOMMUNICATION NUMBER:
TELETAN: 202-508-9190
TELETAN: 202-508-9100
TELETAN: 202-508-9100
TELETAN: 197430 BBBB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 DASA PARIS
TELETAN: 197430 BBBB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 DASA PARIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9600005 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1630 GTGAACGCCGTGGAGATGGCGAG 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     670 ttggccagcgtggtatttgggag 692
Query Match
Best Local Similarity 46.48
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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43..3364
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
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MOLECULE TYPE: C
HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
PCT-US96-00005-1
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; LOCATION:
PCT-US96-00005-1
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                                                                                                                                                                                                                                                                                                                                                    610 cctgacaccttcagggaccagctccaggagctctgcatcccccaagacctggtcggggac 669
                                                                                       agcacgticagaaagtigcigaagtitgiggicagcagccigcagggggggggcigccga 489
                                                                                                                                                                            490 gacggtgtgcagcgtcttggggtcagcgccaacctgccggaggagcagctgggtgcctg
                                                                                                                                                                                                                                                               550 ctggcaggcatgcacacactgctccagcaggccctccgtctgccccccaccagcctgaag
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APPLICANT: ISHIDA, YASUMASA
APPLICANT: SHINOHARA, TAKASHI
ITITLE OF INVENTION: A NOVEL PEPTIDE RELATED TO HUMAN
TITLE OF INVENTION: PROGRAMMED CELL DEATH AND DNA ENCODING IT
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Length 3435;
Score 37.4; DB 6; Length 3 Pred. No. 0.83; 0; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 5524/1994
FILING DATE: 01-MAR-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1630 GIGAACGCCGIGGAGAIGGCGAG 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08396650 Patent No. 5629204
                                                                                                                                                                                                                                                                                                                                                                                                                                         670 ttggccagcgtggtatttgggag 692
Query Match 2.8%;
Best Local Similarity 46.4%;
Matches 122; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 864 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE:
US-08-396-650-2
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DB 1; Length 864;

Score 35.8; D Pred. No. 1.2;

2.68;

Query Match Best Local Similarity

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APPLICANT: ISHIDA, KASUMASA
APPLICANT: SHINOHARA, TAKASHI
ITLE OF INVENTION: A NOVEL PEPTIDE RELATED TO HUMAN
ITLE OF INVENTION: PROGRAMMED CELL DEATH AND DNA ENCODING IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.8; DB 2; Length 864;
Pred. No. 1.2;
0; Mismatches 92; Indels
    Indels
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    92;
    0; Mismatches
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APPLICATION NUMBER: US/08/768,626
FILING DATE: 01-MAR-1995
CLASSIFICATION A135
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 5524/1994
FILING DATE: 01-MAR-1994
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 18904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08768626 Patent No. 5698520 GENERAL INFORMATION:
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TELEX: 6491103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.79
         91; Conservative
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STRANDEDNESS: single
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ADDRESSEE: SUGHRUE,
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US-08-768-626-2
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         Matches
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457 gtggtcagcagcctgcaggggaggactgccgagacggtgtgcagcgtcttggggtcagc 516
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                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HONDO, TASUKU
APPLICANT: HONDO, TASUKU
APPLICANT: SHIDDA, YASUMASA
APPLICANT: SHINDHARA, TAKASHI
TITLE OF INVENTION: A NOVEL PEPTIDE RELATED TO HUMAN
TITLE OF INVENTION: PROGRAMMED CELL DEATH AND DNA ENCODING IT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by similarity to some other pattern
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to an established consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,650
                                                                                                                                                                                                                                                                                                                                                       SUGHRUE, MIGN, ZINN, MACPEAK & SEAS
2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/396,650
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 5524/1994
FILING DATE: 01-WAR-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7860
TELEFAX: (202)293-7860
TELEXAX: (202)293-7860
TELEXAX: (202)293-7860
TELEXAX: (201)293-7860
                                                                                                                           ; Sequence 4, Application US/08396650
; Patent No. 5629204
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nucleic acid
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; IDENTIFICATION METHOD:
US-08-396-650-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig_peptide LOCATION: 25..84
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ZIP: 20037-3202
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                              Washington
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STRANDEDNESS:
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                454 GTG 456
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STREET: 2
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                                            577 caggecetecgtetgeececeaceageetgaageetgaeecetteagggaeeageteeag
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HONJO, TASUKU
APPLICANT: ISHIDA, YASUKU
APPLICANT: ISHIDA, YASUKASA
APPLICANT: SHINOHARA, TAKASHI
ITILE OF INVENTION: A NOVEL PEPTIDE RELATED TO HUMAN
ITILE OF INVENTION: PROGRAMMED CELL DEATH AND DNA ENCODING IT
CORRESPONDENCES:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.8; DB 1; Length 921;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,650
FILING DATE: 01-MAR-1995
CLASSTFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 55224/1994
FILING DATE: 01-MAR-1994
FILING DATE: 01-MAR-1994
FILING DATE: 01-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08396650 Patent No. 5629204 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.6%;
Best Local Similarity 49.7%;
Matches 91; Conservative (
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(202)293-7860
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TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
US-08-396-650-3
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CITY: Washington
STATE: D.C.
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ZIP: 20037-3202
                                                                                                                                       637 gag 639
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Search completed: May 15, 2000, 01:51:08
Job time: 10856 sec
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                                                                           Gaps
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US-08-768-626

Sequence 3, Application US/08768626

Sequence 3, Application US/08768626

Sequence 3, Application US/08768626

GENERAL INFORMATION:

APPLICANT: SHINDHARA, TARASHI

TITLE OF INVENTION: PROGRAMMED CELL DEATH AND DNA ENCODING IT

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: NOW. ZINN. MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

COMPUTER READABLE FORM:

MEDIUM TYPE: Eloppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC Compatible

OPERATION UNMBER: US/08/768,626

FILING DATE: 01-MAR-1995

CLASSTEATION NUMBER: JUS/08/768,626

FILING DATE: 01-MAR-1994

CLASSTEATION NUMBER: JP 5524/1994

FILING DATE: 01-MAR-1995

CLASSTEATION NUMBER: JP 5524/1994

FILING DATE: 01-MAR-1995

TELECOMMUNICATION NUMBER: JP 55224/1994

FILING DATE: 01-MAR-1995

TELECOMMUNICATION NUMBER: JP 55224/1994

FELECOMMUNICATION NUMBER: JP 55224/1994
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Pred. No. 1.2;
0; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : TELEX: 6491103
: INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERESTICS: LENGTH: 921 base pairs ; TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Bost Local Similarity 49.7%;
Watches 91; Conservative
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US-08-768-626-3
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 15, 2000, 02:06:06; Search time 38.86 Seconds (without alignments) 136.533 Million cell updates/sec

US-09-223-796-4 1132 1 MSAVGAATPYLHHPGDSHSG......ALVLKEMADLEKRCERRLQD 224 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963

Total number of hits satisfying chosen parameters:

188963 seqs, 23686106 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Acetyl-CoA-carboxy H. pylori secreted C16N for promoting Rabbit seletal mus Rabbit calcium cha Rabbit skeletal ca Urease accessory m Yeast calcineurin- Rabbit vitronectin Human GC binding p Pisum sativum ACCa
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ALIGNMENTS

RESULT 1 W37723 standard; Protein; 224 AA. DE W37723 standard; Protein; 224 AA. W37723 standard; Protein; 224 AA. W37723 with w37723 standard; Protein; 224 AA. W37723 with w37723 standard; Protein; Regulator. W Wartzeachlular calcium concentration; antibody; hypertension; Article was extracellular calcium concentration; Article woo749807-A2. W W69749807-A2. PR A1-MART P. M W6974997-A2. PR A1-MART P. M W78-M M W78-M M W79-M W79-M M W	QY 121 DEVGDLASVVFGSORPLEDSVAQOQGAWLPHVADFRMRVDVAISTSALARSLQPSVLMQL 180
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181 KLSDGSAYRFEVPTAKFQEURYSVALVLKEMADLEKRCERRLQD 224

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claim 1; Fig 1A-1B; 54pp; English.

Claim 1; Fig 1A-1B; 54pp; English.

Claim 1; Fig 1A-1B; 54pp; English.

This is the amino acid sequence of the human tumourigenesis

This is the amino acid sequence of the human tumourigenesis

This is the amino acid sequence of the human tumourigenesis

This is the amino acid sequence of the human tumourigenesis

This is the amino acid sequence of the human tumourigenesis

This is the amino acid sequence of the human tumourigenesis

is involved with cell proliferation and inflammation. It can be used

to stimulate cell proliferation for deals intended for

to stimulate cell proliferation of tumours or infections, or to treat

a wide range of cancers (adenocarcinoma, melanoma, sarcoma, lymphoma,

c leukaemia etc.), also inflammation where associated with infection or

immunological disease (e.g. asthma, cystic fibrosis, rheumatoid

arthritis). HTAP is also used to raise antibodies are used as for

clasmosis or monitoring of HTAP related diseases (in usual

immunoassays), in competitive drug screens and to isolate HTAP from

its natural sources. HTAP derived probes or primers, are used in

c standard amplification or hybridisation tests to diagnose HTAP-related

diseases; to identify related sequences; for genomic mapping and for 04-DEC-1998 (first entry)
Amino acid sequence of the human tumourigenesis associated protein.
Human: funuourigenesis associated protein: HTAP: transplantation:
tumour: Antagonist; cancer: inflammation: immunological disease;
antibody; probe: primer: PCR: amplification: hybridisation: New tumorigenesis-associated protein and related nucleic acid, vectors, transformed cells - antibodies, agonists and antagonists, for diagnosis, treatment and prevention of abnormal cellular Length 195; Indels 57; DB 1; 8.3%; Score 93.5; DB 22.8%; Pred. No. 0.03; iive 28; Mismatches 204 VAL-----VLKEMADLEKRCERRLQ 223 170 CSMEQLQDLVGKLKDASKSLERATQ 194 Y07867 standard; Protein; 196 AA. screening for specific inhibitors W71684 standard; Protein; 195 AA 20-MAR-1998; U06066. 20-MAR-1997; US-822260. (INCY-) INCYTE PHARM INC. Conservative Hillman JL; Query Match Best Local Similarity Matches 33; Conserv Goli SK, Hillman JI WPI; 98-521224/44. 195 AA Homo sapiens. WO9841635-Al. 24-SEP-1998. N-PSDB; V58281 inhibition Y07867; RESULT W71684

ŝ 06-JUL-1999 (first entry)
Human secreted protein fragment encoded from gene 16.
Human; secreted protein; freatment; prevention; protein therapy; AIDS; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; 71 LEAGKHRADKSTL---STYLEDCKFDRERIELFCTEYQNNKNSLEILLGS------ 118 144 QOGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRYS 203 85 LLAGMHTLLQQALRLPPTSLKPDTF-RDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQ 143 Gaps 27; RESULT X E D A S 셤 ð

proteins uescribes novel isolater numeral years are unsected for proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or green therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Secretic uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal diseases of the immune system, altergies, Alzheimer's and cognitive disorders, schizophrenia, prostate calsestes, settled or cardiac muscle disorders, pulmonary disorders, cransplant rejection, disorders involving osteoclasts such as created in 197852-107993 and the encoding nucleic acids are represented in 197852-107993 and the encoding nucleic acids are represented in 196 AA; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; alleryy, alleryd, alleryd, as diseases; schizophrenia; cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis; arthritis; malignancy; digestive; endocrine; infection. New isolated human genes and the secreted polypeptides they encode Claim 1b; Page 285-286; 368pp; English. This invention describes novel isolated human genes and the secreted Carter KC, Duan DR, Endress GA, Feng P, Ferrie AM, Florence KA, Greene JM, Janat F, Lafleur DW, Ni J, Rosen CA, Ruben SM, Shi Y, Young P, Yu G; (HUMA-) HUMAN GENOME SCI INC. Carter KC, Duan DR, Endress G US-060837. US-060838. US-060839. US-060833. US-060843 02-OCT-1997; US-060874 02-OCT-1997; US-060866 US-060884 99-264022/22. Homo sapiens. WO9918208-A1. 02-0CT-1997; **15-APR-1999** N-PSDB NAMES OF STREET OF STREET

LLAGMHTLLQQALRLPPTSLKPDTF-RDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQ 143 | |||: | ||: | ||: | ||: || ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: QQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRYS 203 Gaps 27; DB 1; Length 196; Indels 57; 8.3%; Score 93.5; DB 22.8%; Pred. No. 0.03; iive 28; Mismatches Conservative Similarity Query Match Best Local Simi. Matches 33; 82 g g ò ð

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W06320; 07-FEB-1997 (first entry) Human mitogen-activated protein kinase kinase 4-alpha. 204 VAL-----VLKEMADLEKRCERRLQ 223 Ą W06320 standard; Protein; 363 170 ò 셤 BASB

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13;
                                                                                                                                                                                                                                                                                                                                                                                                            New mitogen activated protein kinase kinase - useful for treating trachamic heart disease, kidney failure etc., also for identifying modulators for treatment of similar conditions

Claim 11; Fig. 104pp: English.

(WMK4-alpha) (W06320) has serine, threonine and tyroshne kinase activity, and mediates a signal transduction pathway that activates activity, and mediates a signal transduction pathway that activates activity, and mediates a signal transduction pathway that activates activity and activate protein (MAP) kinases p38 and JNK. It is an alternatively spliced form of MKK4-amma (W06322) and MKK4-beta (W06321) isoforms, which differ slightly at the NH2-terminus. MKK4 muscie. Recombinant MKK4 can be produced in transformed host cells.

Claim 12; Fig. 105pc 105pc
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Mitogen-activated protein kinase kinase 4-alpha; MKK4-alpha; MAP; tyrosine kinase; signal transduction; cytokine; oncoprotein;
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10-70.7.
Human mitogen activated protein kinase kinase MKK4 alpha.
MKK4 alpha; human; mitogen activated protein kinase kinase;
MAP kinase kinase; signal transduction; inflammation; psoriasis;
AIDS; cancer; apoptosis; therapy.
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                                                 stress; diagnosis; therapy
                                                                                                                           26-JAN-1996; U01078.
19-MAY-1995; US-446083.
19-SEP-1995; US-530950.
(DAVI,) DAVIS R J.
(DERI/) DERIJARD B.
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Why: 99-L20V/1/LOV

New isolated mitogen-activated protein kinase kinase isoforms - used new isolated mitogen-activated protein kinase kinase isoforms - used to develop products for treating e.g. inflammatory disorders.

Py to develop products for treating e.g. inflammatory disorders.

Py axidative damage, proliferative disorders or autoimmune disorders oxidative damage, proliferative disorders.

CC This polypeptide comprises human mitogen activated protein (MAP)

CC Alnase kinase 4 alpha (MKK4 alpha, beta (see W97671) and gamma or compact of the collect 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 AYGSVNKMVHKP----SG------QIMAVKRIRSTVDEKEQKQLLMDLDVVMRSS 120
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Human mitogen-activated protein kinase kinase 4-beta.

Mitogen-activated protein kinase kinase 4-beta; MKK4-beta; MAP;

tyrosine kinase; signal transduction; cytokine; oncoprotein;

stress; diagnosis; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 82; DB 1; Length 363; 20.2%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 DC------RDG----VQRLGVSAN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                      Davis RJ, Tournier C, Whitmarsh A; WPI; 99-120771/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W06321 standard; Protein; 393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
  UNIV MASSACHUSETTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-1996; U01078.
19-MAY-1995; US-446083.
19-SEP-1995; US-530950.
(DAVI/) DAVIS R J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAINGEAUD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUPTA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
WO9636642-A1.
21-NOV-1996.
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Davis RJ,
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88888888888888888
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                                     New mitogen activated protein kinase kinase - useful for treating ischaemic heart disease, kidney failure etc., also for identifying ischaemic heart disease, kidney failure etc., also for identifying rischaemic heart disease, kidney failure etc., also for identifying modulators for treatment of similar conditions

25 Claim 15; Fig 7: 104ppp: English.

26 Novel human mitogen activated protein kinase kinase 4-beta

27 Novel human mitogen activated protein (MAP) kinases p38 and JNK. It is cativity, and mediates a signal transduction pathway that activates

28 On a leman mitogen-activated protein (MAP) kinases p38 and JNK. It is an alternatively spliced form of MKK4-gamma (W06322) and MKK4-alpha or is expressed in all tissues tested, but partic. In skeletal

29 NKKS (W06318-22) can be used in the treatment of MKK-related disorders, e.g. ischaemic heart disease and kidney failure, to dentify modulators of MKK activity, and to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                  106 AYGSVNKMVHKP----SG-----OIMAVKRIRSTVDEKEQKQLLMDLDVVMRSS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 DCPYIVQFYGALFREGDCWICMELMSTSFDKFYKKVVYSVLDDVIPEEILGKITLATVKAL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LOQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 PHVADFR-----KRVDVAISTSALARSLQP---SVLMQL-----K 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 PYMAPERIDPSASRQGYDVRSDVWSLGITLYELATGRFPYPKWNSVFDQLTQVVKGDPPQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wew isolated micogen-activated protein kinase kinase isoforms - used to develop products for treating e.g. inflammatory disorders, oxidative damage, proliferative disorders or autoimmune disorders Example 1; Page 135-136; 168pp; English.

This polypeptide comprises human mitogen activated protein (MAP) kinase kinase 4 beta (MKK4 beta). Its sequence was deduced from a cDNs clone (see X7008) derived from human brain mRNA. MKK4 includes 3 isoforms, termed MKK4 alpha (see W97670), beta and gamma (see W97672), that vary slightly at the N-terminus. MKK4 is a p38
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DC-------RDG-----VQRLGVSAN-------LPEEQLGAL-LAGMHTL 92
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                      3 AVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1999 (first entry)
Human mitogen activated protein kinase kinase MKK4 beta.
MKK4 beta: human: mitogen activated protein kinase kinase;
MAP kinase kinase; signal transduction; inflammation; psoriasis;
AIDS; cancer; apoptosis; therapy.
                                                                                                                                                                                                                                                                                                                                                           Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSNSEEREFSPSFINFVNLCLTKDESKRPKYKELLKHPFILMYEERAVEVAC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 LSDGSAYRF-------EVPTAKFQELRYSVALVLKEMADLEKRC 218
                                                                                                                                                                                                                                                                                                                          7.2%; Score 82; DB 1; Length 393; 20.2%; Pred. No. 1.2; Live 44; Mismatches 89; Indels
 Raingeaud J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-1999.
07-JUL-1998: U14101.
07-JUL-1997; US-888429.
(UYMA-) UNIV MASSACHUSETIS.
Davis RJ, Tournier C, Whitmarsh A;
WPI; 99-120771/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W97671 standard; Protein; 393 AA.
   Gupta S,
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 20.2% Matches 59; Conservative
 Davis RJ, Derijard B,
WPI; 97-012035/01.
N-PSDB; T43206.
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MAP kinase kinase that also phosphorylates the JNK subgroup of MAP kinases. MKK3, MKK4, MKK6 and MKK7 (see W97664 and W97668-72), described in the invention, mediate the transduction of specific signals from the cell surface to the nucleus along specific pathways. They are useful for screening reagents which modulate MKK activity. Such agents can be used to prevent or treat MKK activity. Such agents can be used to prevent or treat MKK activity of sortismers, e.g. inflammation, oxidative damage or stress related disorders, e.g. inflammation, oxidative damage or alignancies of e.g. the skin, bone marrow, lung, liver, breast, malignancies of e.g. the skin, bone marrow, lung, liver, breast, inhibit the activity or expression of MKK inhibit cell growth or consequence apoptosis. MKK7 polynucleotides (see W07059-64) and sequence 393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 --LOQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AYGSVNKMYHKP----SG------QIMAVKRIRSTVDEKEQKQLLMDLDVVMRSS 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 PYMAPERIDPSASRQGYDVRSDVWSLGITLYELATGRFPYPKWNSVFDQLTQVVKGDPPQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DC------RDG-----VQRLGVSAN------LPEEQLGAL-LAGMHTL 92
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Novel human mitogen activated protein kinase kinase 4-gamma (MKK4-gamma) (W06322) has serine, threonine and troshe kinase activity, and mediates a signal transduction pathway that activates human mitogen-activated protein (MAP) kinases p38 and JNK. Its amino acid sequence was deduced from a cDNA clone (T43206) obtd. from a human foetal brain library. Alternative splicing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mitogen-activated protein kinase kinase 4-gamma.
Mitogen-activated protein kinase kinase 4-gamma; MRK4-gamma; tyrosine kinase; signal transduction; cytokine; oncoprotein; stress; diagnosis; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 393;
1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 82; DB 20.2%; Pred. No. 1.2; ive 44; Mismatches
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Matches 59; Conservative
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19-MAY-1995; US-446083.
19-SEP-1995; US-530950.
(DAVI.) DAVIS R J.
(DERI.) DERIJARD B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAINGEAUD J.
I, Derijard B,
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WO9636642-A1.
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13;
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Example 1; Page 139; 168pp; English.

Kinase kinase damade (mkK4 gamma) Its sequence was deduced from kinase kinase damma (mkK4 gamma). Its sequence was deduced from cloudes 3 isoforms, termed MKK4 alpha (see W97670), beta (see W97671) and gamma, that vary slightly at the N-terminus. MKK4 is a pse MAP kinase kinase that also phosphorylates the JNK subgroup of MAP kinases. MKK3, MKK4, MKK6 and MK7 (see W97664 and W97668-72), castroined in the invention, mediate the transduction of specific pathways. They are useful for screening reagents which modulate CC signals from the cell surface to the nucleus along specific pathways. They are useful for screening reagents which modulate CC stress-related proliferative disorders, e.g. psoriasis, AIDS, castrointestinal system and genito-urinary tract. Agents which complish the activity or expression of MKK inhibit cell growth or cause apoptosis. MKK7 polynucleotides (see X07059-64) and
                                                                                                                                                                                                                                                                                    --LOGALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence yields MKK4 isoforms alpha (W06320) and beta (W06321).
MKK4 is expressed in all tissues tested, but partic. in skeletal
muscle. Recombinant MKK4 can be produced in transformed host cells.
MKKs (W06318-22) can be used in the treatment of MKK.related
disorders, e.g. ischaemic heart disease and kidney failure, to
identify modulators of MKK activity, and to raise antibodies.
                                                                                                                                                                                                                         89; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----WRVDVAISTSALARSLQP---SVLMQL------K 181
                                                                                                                                                                                                                                                       3 AVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGE 62
                                                                                                                                                                                                                                                                                                                                  217 NHLKENLKIIHRDIKPSN------ILLDRSGNIKLCDFGISGQLVDSIAKTRDAGCR
                                                                                                                                                                                                                                                                                                                                                                          157 DCPYIVQFYGALFREGDCWICMELMSTSFDKFYKYVYSVLDDVIPEEILGKITLATVKAL
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Human mitogen activated protein kinase kinase MKK4 gamma.
MKK4 gamma; human; mitogen activated protein kinase kinase;
MAP kinase kinase; signal transduction; inflammation; psoriasis;
AIDS; cancer; apoptosis; therapy.
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                                                                                                                                                                             7.2%; Score 82; DB 1; Length 399; 20.2%; Pred. No. 1.2; ive 44; Mismatches 89; Indels
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07-JUL-1998; U14101.
07-JUL-1997; US-888429.
(UYMA-) UNIV MASSACHUSETIS.
                                                                                                                                                                                                                   59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHVADFR-----
                                                                                                                                                                                                Similarity
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                                                                                                                                                                           Query Match
Best Local S.
Matches 59
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93 --LQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL- 150
                                                                                                                                                         112 AYGSVNKMVHKP----SG-----QIMAVKRIRSTVDEKEQKQLLMDLDVVMRSS 156
                                                                                                                                                                                                                                                                                    217 NHLKENLKIIHRDIKPSN-----ILLDRSGNIKLCDFGISGQLVDSIAKTRDAGCR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 1; 23pp; Japanese.
The polypeptide is recognised by auto-antibodies in the serum of a bullous pemphigoid patient and by a human anti-basement membrane zone monoclonal antibody. It can be used for diagnosis of bullous pemphigoid. See also Q15020.
                                                                                                                                                                                                                                                                                                                                                 268 PYMAPEKIDPSASROGYDVRSDVWSLGITLYELAIGKFPYPKWNSVFDQLIQVVKGDPPQ 327
                                                                                                                           3 AVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 QFRQPGAPLDRESSQPCYSEYFSQTSTELQITFDDKNPITR------LSEL 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 SAFDTAGRECHHPAEISPGNSGHLNLKTRLPLSRWTQEPHQTEGKWPHRAAEQLPKEV-- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 QQQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA which encodes mouse derived bullous pemphigoid antigen protein contg. base sequence which encodes polypeptide composed of specified 996 aminoacid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                    PHVADFR----SVLMQL----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .36 MARILG-DLDRSTFRKLLKFVVSSLQGE-----DCRDGVQRLGVSANLPEEQLGALLAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 HILLQQALR--LPPTSLKPDTFRDQLQELCIPQDLV----GDLASVVFGSQRPLLDSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                                                                   182 LSDGSAYRF------EVPTAKFQELRYSVALVLKEMADLEKRC 218
                                                                                                                                                                                                                                                                                                                                                                                                                 LSNSEEREFSPSFINFVNLCLTKDESKRPKYKELLKHPFILMYEERAVEVAC 379
                                                                     Length 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Length 997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 7.2%; Score 82; DB 1; Length 997 Local Similarity 22.4%; Pred. No. 4.2; les 59; Conservative 30; Mismatches 106; Indels
                                                                                                 89;
                                                                     DB 1;
                                                                 7.2%; Score 82; DB 20.2%; Pred. No. 1.2; ive 44; Mismatches
                                                                                                                                                                                           63 DC------RDG-----VQRLGVSAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1992 (first entry)
Mouse bullous pemphigoid antigen protein.
dermatological syndrome; blisters; murine.
     s (see W97662-67) are claimed.
399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAVGAATPYLHHPGDSHSGRVSFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R15345 standard; Protein; 997
R15345;
                                                           Query Match
Best Local Similarity 20.29
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEF-1991.
09-APR-1990; 093585.
31-OCT-1989; JP-283947.
09-APR-1990; JP-093585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TOFU ) TONEN CORP. WPI; 91-356566/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  997 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           015019
   polypeptides
Sequence 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                   328
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Matches
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Example 2; Column 23-28; 34pp; English.

This sequence is the E. coll 7-keto-8-aminopelargonic acid (KAP)

This sequence is the E. coll 7-keto-8-aminopelargonic acid (KAP)

Synthetrase. The gene can be used in the transpenic plant of the

invention. The transgenic plant, plant cell or plant tissue is

transformed with a chimeric gene encoding diaminopelargonic acid (DAP)

aminotransferase or biotin synthase and produces more biotin than a

non-transgenic plant, cell or tissue. The plant is used as an improved

dietary source of biotin (vitamin H) for humans or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 WLPHVADFRWRVDVAISTSALA-----179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 LPPISLKPDIFRD-----QLQELCIPQDLVGDLASVVF----GSQRPL--LDSVAQQQGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 LSPSQLRRFAHNDVTHLARLLASPCPGQQMV -- VTEGVFSMDGDSAPLAEIQQVTQQHNG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 WL------MVDDAHGTGVIGEQGRGSCWLQXVKPELLVVTFGKGFGVSGAAVLCSSTV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 YSRALLFISGFAANQAVIAAAMAKEDRIAADRLS--------HASLLEAAS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 FRKLLKF------VVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AATPYL---HHP-----GDSHSGRVSFLGAQLPPEVAAMARLLGDLDRST 47
aminotransferase; diaminopelargonic acid; transgenic plant;
in synthase; biotin production; vitamin H; KAP synthetage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene encoding lipase isolated from Pseudomonas SD705 - useful industrially in detergents, food processing and paper and oil
                                                                                                                                                                                                                                                                                                                                         N-PSDB; X01301.
Transgenic, plants with high biotin levels - transformed with Dencoding di:amino-pelargonic acid amino-transferase or biotin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-ARR-1997 (first entry)
29-ARR-1997 (first entry)
Especial control of (FRM BP-4772) lipase.
Lipase; detergent; food processing; paper; oil; manufacture vector; recombinant production; transformed host; SD705; Pseudomonas; alcaligenes; SD702; Bacillus; NKS-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 81.5; DB 1; Length 384;
19.9%; Pred. No. 1.3;
tive 32; Mismatches 90; Indels 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 SSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 ---QLKLSDGSAYRFEVPTAKFQELRYSVALVLKEMADLEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : | : | |: | 152 ADYLLQFARHLIYSTSMPPAQAQALRASLAVIRSDEGDARR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoneda
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Claim 3; Pages 32-34; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥
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                                                                                                                                                                                                                                               (NOVS ) NOVARTIS FINANCE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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27-FEB-1995; JP-038527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHOW ) SHOWA DENKO KK
                                                                                                                                                         30-APR-1997; 846338.
30-APR-1997; US-846338.
08-MAR-1995; US-401068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohno K, Sasuga J,
WPI; 96-412770/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 56; Conserv
         DAP aminotransferas
biotin synthase; bi
Escherichia coli.
US5869719-A.
                                                                                                                                                                                                                                                                                                               WPI; 99-152902/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas sp.
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                                                                                                                                                                                                                                                                                      Patton DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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PP 01-OCT-1993: E02688.

PR 02-OCT-1992: CH-003124.

PR 15-JUL-1993: CH-002134.

PR 15-JUL-1993: CH-00214.

PR 15-JUL-1993: CH-00214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 WLPHVADFRWRVDVAISTSALA-----178LQPSVLM-------179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 YSRALLFISGFAANQAVIAAMMAKEDRIAADRLS---------HASLLEAAS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 WL------MVDDAHGTGVIGEOGRGSCWLQKVKPELLVVTFGKGFGVSGAAVLCSSTV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 LPPTSLKPDTFRD-----OLQELCIPQDLVGDLASVVF---GSQRPL--LDSVAQQQGA 147
                                            441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 FRKLLKF------VVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATPYL---HHP-----GDSHSGRVSFLGAQLPPEVAAMARLLGDLDRST 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLG-----
               KAPA synthase encoded by biof gene in plasmid pB030A-15/9. Blotin: expression, enterobacteria; vitamin H; synthesis; plasmid; pB030A-15/9; bioB; bioF; bioC; bioD; bioA; promoter ptac; biotin synthase; KPAP synthase; B-amino-7-oxononanoate synthase; pimeloyl-CoA; DTB synthase; dethiobiotin synthase; DAPA synthase; S-adenosyl-L-methionine: 8-amino-7-oxononanoate aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.2%; Score 81.5; DB 1; Length 384; 19.9%; Pred. No. 1.3; tive 32; Mismatches 90; Indels 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 --- OLKLSÖGSAYRFEVPTAKFQELRYSVALVLKEMADLEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                            R51884 standard; Protein; 384 AA
                                                                                                                                                                      464
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                                                                                                               203 SVA---LVLKEMADLEKRCERRL
                                                                                                                                                   : | | | : |: | : | | 442 TVTGRQLVEAKLLDMRTVEQLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-1999 (first entry)
E. coli KAP synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 19.99
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seborrhoea; dermatitis.
Escherichia coli DSM498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . W73904;
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RESULT 12

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LMQLKLSDGSAYRFE 191
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    158 RVDVAISTSALA----
                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 38; Conserv
                                                                                                                                                                                                                                                                                                               WPI; 94-048875/06.
                                                                                                                                                                                                                                                                                                                             N-PSDB; Q56106
                                                                                                                                                                      27-JUL-1994
                                                                                                                                                                                                                                                  03-FEB-1994
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid contg. gene(s) for expression of biotin synthetase enzymes - derived from L.coli and capable of replication and expression in other microorganisms, esp. yeast.

Table 6; page 39-40; 52pp; English.

The enzyme is expressed by the E.coli bio F.gene. It is a biotin synthetase enzyme, and permits the transformant to grow in the absence of sequence 383 AA;
                                                                                                                                                                                    270 ALDRORSEWDORLSGFNREROALISOPGLADSDROAAIEALLHEQFSEH-----ER 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLGALLAGMH-TLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLD 139
                                                                                                                                                                                                                                                                      SVAQQQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFRD-----QLQELCIPQDLVGDLASVVF---GSQRPL-LDSVAQQQGAWLPHVADFRW 157
                                                                                                                                            34; Gaps
                                                                                                                                                                   RVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEE 80
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The present sequence is a lipase isolated from Pseudomonas sp. 20705 (FBRM BP-4772), which is industrially useful in detergents, food processing, paper manufacture and oil manufacture, etc. . A vector containing the lipase gene can be used for the recombinant production of the lipase in transformed hosts, especially Pseudomonas 20705, P. alcaligenes SD702 or Bacillus NKS-21. Sequence 335 AA;
                                                                                                                                                                                                                                              223 LOGLLVPOLHLTLRQQTQQLLEQGAEP----EQLRQLRL--NLVGPQAT-----ERLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
                                                                                                                Query Match 7.2%; Score 81; DB 1; Length 335; Best Local Similarity 24.9%; Pred. No. 1.3; Matches 50; Conservative 32; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 383;
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Pred. No. 1.5;
1; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-1990 (first entry)
Peptide expressed by E.coli Bio F gene.
E.coli; Bio F; biotin.
Escherichia coll.
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21.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.2%
Best Local Similarity 21.0°
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-1989.
17-MAR-1989; 006210.
22-MAR-1988; GB-006804.
17-MAR-1989; GB-006210.
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WPI; 89-295085/41.
N-PSDB; N91333.
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-QLKLSDG 185
                                             201 MVDDAHGTGVIGEQGRGSCWLQKVRPELLVVTFGKGFGVSGAAVLCSSTVADYLLQFARH 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 CIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWLPHVADFRWRVDVAISTSALARSLQPSV 176
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The lipase gene from Pseudomonas pseudoalcaligenes MI was cloned is 2. coli as in Ep-334462. The DNA sequence of insert Pvul/Econt contains two open reading frames, one encoding the lipase gene, the other encoding a putative lipase modulator gene which increases the lipase productivity in a homologous host cell. The lipase obtd. is detergents or diagnostic reagents.

See also R47212.
                                                                                                                                                                                                                                                                                                                                                       Lipase modulator.

Seudomonas; cloning; lipase gene; lipase modulator gene; lipids; oils; fats; detergents; diagnostic reagents.

Pseudimonas pseudoalcaligenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 79.5; DB 1; Length 344; 28.1%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing lipase prodn. in Pseudomonas species - by clon.
Lipase gene and a lipase modulator gene into a homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
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                                                                                                                                   186 SAYRFEVPTAKFQELRYSVALVLKEMADLEK
--RSLQPSVLM-
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                                                                                                                                                                                                                                                                          R47213 standard; Protein; 344
R47213;
                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-1993; E01995.
23-JUL-1992; EP-202281.
(KONN ) GIST-BROCADES NV.
COX MMJ, Gerritse G, Qu
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 265569
US-08-822-260-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.5
Best Local Similarity 20.8
Matches 43; Conservative
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Sequence 2, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 53, Appl
                                                                          May 15, 2000, 03:22:30 ; Search time 35.18 Seconds (without alignments) 92.094 Million cell updates/sec
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Sequence 3, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 6, Appli
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                                                                                                                                US-09-223-796-4
1132
1 MSAVGAATPYLHHFGDSHSG......ALVLKEMADLEKRCERRLQD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, p
Sequence 5, p
Sequence 5, p
Sequence 9, p
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                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-822-260-1
US-08-530-950-6
US-08-874-186-92
US-08-440-068-2
US-08-440-068-2
US-08-875-062-3
US-08-875-062-3
US-08-875-062-3
US-08-870-950-8
US-08-223-305C-53
US-08-223-305C-53
US-08-233-52-27
US-08-233-22-27
US-08-233-22-27
US-08-338-227-8
US-08-338-257-8
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US-08-795-303-18
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US-08-434-998-9
US-08-487-797-9
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US-09-015-815-1
                                                                                                                                                                                                                               143561 seqs, 14463640 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Maximum DB seq length: 1000000
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Perfect score:
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82
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Sequence 9, Appli Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 74, Appl Sequence 6, Appli Sequence 78, Appl Sequence 78, Appl Sequence 2, Appli Sequence 2, Appli		
PCT-US95-02058-9 US-08-357-598-11 US-09-003-289-11 PCT-US95-16435-11 US-08-559-3038-74 US-08-559-3038-74 US-08-559-3038-78 US-08-559-3038-78 US-08-559-3038-78 US-08-660-836-4 US-08-660-836-4 US-08-6449-5 US-08-447-500-2 US-08-447-500-2 US-08-447-408-2	ALIGNMENTS	US/08822260 Jennifer L. 'ya K. NOVEL TUMORIGENESIS PROTEIN SISTANTIACCUTICALS, INC. IT Drive TO WINDOWS VERSION 2.0 FOR WINDOWS VERSION 2.0 Ith A: AI.
55.0 5.9 11000 5.9 11000 5.9 11000 5.9 11000 5.9 11000 5.9 11000 5.9 11000 5.9 5.9 5.9 5.9 5.9 5.9 5.9 5.9		TO DE COME CONTROL OF THE PROPERTY OF THE PROP
330 310 311 312 313 313 313 313 314 314 316 317 318 319 319 319 319 319 319 319 319		US-08-822-260-3 US-08-822-260-3 Sequence 3, Application US Patent No. 583666 APPLICANT: Hillman, Je APPLICANT: Goli, Surya APPLICANT: Goli, Surya APPLICANT: Goli, Surya TILLE OF INVENTION: US CORRESPONDENCE ADDRESS: 3 CORRESPONDENCE ADDRESS: 3 CORRESPONDENCE ADDRESS: 3 COUNTY: Dalo Alto SITRET: 3174 Porter CITY: Palo Alto SITRET: BALO ALTO COUNTY: USA ZIP: 94364 COUNTY: USA ZIP: 94364 COUNTY: USA
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Gaps

54;

8.5%; Score 96; DB 2; Length 195; 20.8%; Pred. No. 0.0017; .ive 32; Mismatches 78; Indels

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144 QOGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRYS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----WRVDVAISTSALARSLOP---SVLMQL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/530,950 FILLING DATE: 19-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.2%; Score 82; DB 1
Best Local Similarity 20.2%; Pred. No. 0.2;
Matches 59; Conservative 44; Mismatches
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                                                                                                                         170 CSMEQLQDLVGKLKDASKSLERATQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: FASSE, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH; 363 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                     Sequence 6, Application US/08530950
Patent No. 5736381
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
                                                                                       204 VAL----VLKEMADLEKRCERRLQ
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MEDIUM TYPE: Floppy
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 LEAGKHRADKSTL---STYLEDCKFDRERIELFCTEYQNNKNSLEILLGS------ 118
                                                                                                                                                                               142 AQQQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKL--SDGSAY---RFEVPTAK 196
                                                                                              ------PDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSV 141
                                                                                                                              56 PVVLKHCHAAAATCILEAGKHQVDKSTLSTYLEDCKFDRERI-ELFCTEYQNNKNSLETL 114
         GDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLP 100
                                                                                                                                                                                                            115 LGSIGRSLPHITDVSWRLEYQIKTNQLHKMYRPGYLVTLNVENNDSQSYPEINFSCNMEQ
                                                 18 GSFDSNAFALLLRAAFQSL------LDARADEAALD-----HPYLKQ---ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL TUMORIGENESIS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
PILING DATE: Herewith
                                                                                                                                                                                                                                                                         197 FQELRYSVALVLKEMADLEKRCERRLQ 223
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ATTORNEYAGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08822260 Patent No. 5830660 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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; CLONE: 2267574
US-08-822-260-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
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                                                                                                   101 PTSLK-----
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13; 121 DCPYIVQFYGALFREGDCWICMELMSTSFDKFYKYVYSVLDDVIPEEILGKITLATVKAL 180 93 --LQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL- 150 63 DC------RDG----VQRLGVSAN------LPEEQLGAL-LAGMHTL 92 3 AVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGE 62 APPLICANT: Gupta, Shashi
APPLICANT: Gupta, Shashi
APPLICANT: Derijard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street Indels 100;

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APPLICANT: Teng, David H-F.
APPLICANT: Taviijan, Sean V.
APPLICANT: Taviijan, Sean V.
APPLICANT: Perry III, William L.
APPLICANT: Scholick, Mark H.
AIMKK4) IN HUMAN TUMOR CELL LINES IDENTIFY IT AS A TUMOR TITLE OF INVENTION: SUPPRESSOR IN VARIOUS TYPES OF CANCER
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, ILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 NHLKENLKIIHRDIKPSN-----ILLDRSGNIKLCDFGISGQLVDSIAKTRDAGCR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 PYMAPERIDPSASROGYDVRSDVWSLGITLYELAIGRFPYPKWNSVFDQLIQVVKGDPPQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------WRVDVAISTSALARSLQP---SVLMQL------K 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 DC------RDG-----VQRLGVSAN-------LPEEQLGAL-LAGMHTL
                                      | | : | :: | :: | :| | | 328 LSNSEREFSPSFINFVNLØLTKDESKRPKYKELLKHPFILMYEERAVEVAC 379
                 --EVPTAKFQELRYSVALVLKEMADLEKRC 218
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Venable, Baetjer, Howard & Civiletti,
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 82; DB;
20.2%; Pred. No. 0.23;
ive 44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,482
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     Sequence 92, Application US/18874186
Patent No. 5989885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2481
TELEPHONE: 202-962-4848
NEDAMY: 202-967-671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-874-186-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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            182 LSDGSAYRF--
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ZIP: 20005
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232 PYMAPERIDPSASRQGYDVRSDVWSLGITLYELATGRFPYPKWNSVFDQLJQVVKGDPPQ 291
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Davis, Roger J.
APPLICANT: Baingeaud, Joel
APPLICANT: Gupta, Shash!
APPLICANT: Derijard, Benoit
TITLE OF INVENTION: CYTORINE, STRESS-, AND
TITLE OF INVENTION: NICOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                    ---EVPTAKFQELRYSVALVLKEMADLEKRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 82; DB 1; Length 399; 20.2%; Pred. No. 0.23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
STATE: MA
COUNTRY: USA
ZIP: 0210-2804
ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FLOPPY disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/01001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
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                                                                                                                                                                                   Sequence 10, Application US/08530950 Patent No. 5736381
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 20.2°
Matches 59; Conservative
                                        182 LSDGSAYRF----
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STRANDEDNESS: no
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                                                                                                                                                          US-08-530-950-10
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FILING DATE:
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US-08-846-338-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 WL------MVDDAHGİGVIGEQGRGSCWLOKVKPELLVVTFGKGFGVSGAAVLCSSTV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 LPPTSLKPDTFRD-----QLQELCIPQDLVGDLASVVF---GSQRPL--LDSVAQQQGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 YSRALLFISGFAANQAVIAAMMAKEDRIAADRLS--------HASLLEAAS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 SSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLG----- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 FRKLLKF------VVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AATPYL---HHP-----GDSHSGRVSFLGAQLPPEVAAMARLLGDLDRST 47
                                                                                                                                                                                                                      Enhanced Biotin Biosynthesis in Plant Tissue
  --EVPTAKFQELRYSVALVLKEMADLEKRC 218
                                     328 LSNSEEREFSPSFINFVNLCLTKDESKRPKYKELLKHPFILMYEERAVEVAC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%; Score 81.5; DB 2; Length 384;
19.9%; Pred. No. 0.25;
ive 32; Mismatches 90; Indels 10.
                                                                                                                                                                                                                                                                                                                                                                                               COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 ---QLKLSDGSAYRFEVPTAKFQELRYSVALVLKEMADLEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 ADYLLQFARHLIYSTSMPPAQAQALRASLAVIRSDEGDARR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,970
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTATION NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFRX: 919-541-8689
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Enhanced Biotin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
SIREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 WLPHVADFRWRVDVAISTSALA----
                                                                                                                                       Sequence 2, Application US/08401068 Patent No. 5859335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 384 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-401-068-2
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Matches 56; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                              USA
    182 LSDGSAYRF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         STATE: N'COUNTRY:
                                                                                                                        US-08-401-068-2
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Transgenic Plants Having Increased Biotin Content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 WL------MYDDAHGTGVIGEQGRGSCWLQKVKPELLVVTFGKGFGVSGAAVLCSSTV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AATPYL---HHP-----GDSHSGRVSFLGAQLPPEVAAMARLLGDLDRST 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 SSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLG----- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YONEDA, TADASHI
APPLICANT: HARUM, TAKADA
APPLICANT: HARUM, TAKADA
APPLICANT: KEI, OHNO
APPLICANT: JUNIJ, SASUGA
TITLE OF INVENTION: NOVEL LIPASE GENE AND PROCESS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 --- QLKLSDGSAYRFEVPTAKFQELRYSVALVLKEMADLEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
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0.25;
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: 0. 05869719artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --RSLQPSVLM-
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19.9%; Pred. No. 0.25
iive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/846,338
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                                                                                                                                                                                                                                                                                                                                                                  STEEET: 520 White Plains Road, CITY: Tarrytown STATE: NY COUNTY: USA 21P: 10591 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC competible COMPUTER: IBM PC comPUTER: IBM PC comPUTER: IBM PC comPUTER: IBM PC c
Sequence 2, Application US/08/046338
Patent No. 5869719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 WLPHVADFRWRVDVAISTSALA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 384 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 19.9%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                            GENERAL INFORMATION:
APPLICANT: Patton,
TITLE OF INVENTION:
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259 GCRPYMAPERIDFSASRQGYDVRSDVWSLGITLYELATGRFPYPKWNSVFDQLTQVVKGD 318
                                                                                                                                                                                                                                                                                                 3 AVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGE 62
                                                                                                                                                                                                                                                                                                                                                                                         US-08-606-888A-5

Sequence 5, Application US/0860688A

Fatent No. 5766913

Fatent No. 5766913

Fatent No. 5766913

APPLICANT: Lin, Shuen-Fuh

APPLICANT: Chiou, Chien-Ming

APPLICANT: Chiou, Chien-Ming

TITLE OF INVENTION: CLONING, EXPRESSION AND NUCLEOTIDE

TITLE OF INVENTION: SEQUENCE OF A RALINE GENE FROM PSEUDOMONAS

TITLE OF INVENTION: PSEUDOALCALIGENES F-111

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flab & Richerts

STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 --LQQALRLPPTSLKPDTF---RDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 -----WLPHVADFR-------WRVDVAISTSALARSLQP---SVLMQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- EVPTAKFQELRYSVALVLKEMADLEKRC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 PPQLSNSEEREFSPSFINFVNLCLIKDESKRPKYKELLKHPFILMYEERAVEVAC 373
                                                                                                                                                                                                           Query Match 7.0%; Score 79; DB 1; Length 393; Best Local Similarity 20.0%; Pred. No. 0.5; Matches 59; Conservative 42; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USE

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDLUM TYEE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/606,888A

FILING DATE: 26-FEB-1996

***SCTFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06840/003001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: ISAO, ROCKY Y.
REGISTRATION NUMBER: 34,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                     not relevant
         ; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acids
; STRANDEDNESS: not relevant
US-08-530-950-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 --KLSDGSAYRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617/542-8906
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STREET: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 SVAQQQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 RVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Davis, Roder J.
APPLICANT: Raingeaud, Joel
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shout
APPLICANT: Gupta, Shout
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: PRODUCTION OF LIPASE WITH THE USE OF THE SAME
                                                                                                                                                                                                                                                                                                                                        Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 ALDRORSEWDORLSGFNREROAIISOPGLADSDKQAAIEALLHEOFSEH---
                                                                                                                                                                                                                                                                                                                                                                                  85; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                               Ouery Match 7.2%; Score 81; DB 2;
Best Local Similarity 24.9%; Pred. No. 0.23;
Matches 50; Conservative 32; Mismatches
                  FILE REFERENCE: 5059.204
CURRENT APPLICATION NUMBER: US/08/875,062B
CURRENT FILING DATE: 1997-07-10
EARLIER APPLICATION NUMBER: PCT/JP96/00426
EARLIER FILING DATE: 1996-02-23
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fasse, J. Peter
RECISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMBUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-SEP-1995
CLIACASIFICATION: 435
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08530950 Patent No. 5736381 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 LRVS-----SLLGLDSRAER 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 LRYSVALVLKEMADLEKRCER 220
                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas sp
US-08-875-062-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 FI
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                  LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                        238 LHLTLRHDPAVADQGAEPEQLRQLRLNLFGPQATERLERLDRQRSEWDQRLERFNRERQA 297
                                                                                                                                                                                                                24 FLGAQLPPEVAAMARLLGDLDRSTFRK--LLKF-----VVSSLQGEDCR-DGVQRLGVSA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harpold, Michael
APPLICANT: Elis, Steven
APPLICANT: Elis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McGue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ANDRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 VAQQQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 77; DB 1; Length 340;
26.2%; Pred. No. 0.69;
tive 23; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                     76 NLPEEQLGALLAGMHTLLQQALR----LPPTSLKPDT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Brown, Martin, Haller & McClain STREET: 1660 Union Street CITY: San Diego STATE: California COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FESTERO VECKSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: APIL 4, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: APIL 10, 1992
PRIOR APPLICATION NUMBER: US 07/868,354
FILING DATE: 15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/603,751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                          Matches 60; Conservative
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-8888A-5
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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606 TXTWIPVNGID-----YSLALVLPIYSFYXIKAKLEETIIQA-RYSET-LKRDNFEES 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PYLHHPGDSHSGRVSFLGAQLPPEVAAMAR---LLGDLDRSTFRKLLK----- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
APPLICANT: Wccue, Ann M
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
6.3%; Score 71.5; DB 1; Length 1103;
Best Local Similarity 23.1%; Pred. No. 18;
Matches 31; Conservative 19; Mismatches 59; Indels 25
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEPAX: (619)238-0969
TELEPAX: (619)238-0062
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/223,305C
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 53, Application US/08223305C; Patent No. 5851824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LOELCIPODLVGDL 126
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-223-305C-53
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72 GVSANLPEEQLGAL----LAGMHTLL-----QQALRLP-----PTSLKPDŢFRDQL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 HPGDSHSGRVSFL-GAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Variance of the control o
                                                             ZIP: 90017-2571
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,822C
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 70.5; Di
26.0%; Pred. No. 6.9;
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                              ATTORNET/AGENT INFORMATION:
NAME: Churchili, Margaret A. (Ph.D.)
RECISTRATION NUMBER: 9,944
REFERENCE/DOCKET NUMBER: 1279-194XX
TELEPHONE: 213/892-9200
TELEPHONE: 213/680-4518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 27, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 27:
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Best Local Similarity 26.0%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS LENGTH: 489 amino acid
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                 California
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HYPOTHETICAL: N
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US-08-369-822C-27
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Patent No. 6015660
GENERAL INFORMATION:
APPLICANT: Lipkin, W. I.
APPLICANT: Kliche, Stefanie
APPLICANT: Schneider, Patrick A.
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 -FVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     606 TYTWTPVNGID-----YSLALVLPTYSFYYIKAKLEETITQA-RYSET-LKPDNFEES 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
           6.3%; Score 71.5; DB
23.1%; Pred. No. 18;
tive 19; Mismatches
April 10, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619)238-0052
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 1103 amino acids
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Best Local Similarity 23.1%
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 LQELCIPQDLVGDL 126
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IBM Compatible (YSTEM: DOS FastSEQ Version 1.5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williams, Mark E.
APPLICANT: Harpold, Michael Miller
APPLICANT: Benwartz, Arnold
APPLICANT: Schwartz, GCCIUM CHANNEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CONTRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
STATE: CA
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
6.2%; Score 70.5; DB 1; Length 3218;
Best Local Similarity 22.1%; Pred. No. 1.2e+02;
Matches 58; Conservative 41; Mismatches 94; Indels 69
                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
FILING DATE: 17. MAR-1993
PRILING DATE: 17. MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5773700118.
REGISTRATION NUMBER: 34,490
REGISTRATION NUMBER: 34,490
REFERENCE/OCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3218 amino acids
APPLICATION NUMBER: US/08/764,100 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08435675B Patent No. 5710250
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ellis, Steven Bradley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3055 ALALEALATYRLECYSSERILE 3076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-764-100-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92101-2926
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-435-675B-5
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548 PNVQNPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVK-------SQDER 600
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23.7%; Pred. No. 28;
tive 18; Mismatches 59; Indels
CURRENT ARELICATION DATA:
APPLICATION NUMBER: US/08/435,675B
FILING DATE: 05-MAY-1995
CLASSIFICATION NUMBER: US/08/436,675B
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/314,083
FILING DATE: 28-SEP-1994
APPLICATION NUMBER: US 07/603,751
FILING DATE: 08-NOY-1990
ATTORNEY AGENT INFORMATION:
NAME: Seldmen: Stephenie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53193
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-238-099
TELEFAX: 619-238-099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 15, 2000, 03:22:32
Job time: 5778 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 32; Conserva
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FRAGMENT TYPE:
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 protein search, using sw model OM protein

Run on:

May 15, 2000, 03:23:35; Search time 52.16 Seconds (without alignments) 251.784 Million cell updates/sec

US-09-223-796-4 1132 Perfect score:

1 MSAVGAATPYLHHPGDSHSG.....ALVLKEMADLEKRCERRLQD Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

168808 seqs, 58629743 residues Searched:

Total number of

168808 hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_63:* 1: pir1: 2: pir2: 3: pir3: 4: pir4: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

230k bullous pemph 8-amino-7-oxonoan 3',5'-cyclic-GMP p nuclear pore membr importin beta-1 su calcineurin inhibi hypothetical prote heat shock protein hypothetical prote pfes protein - Pse beta-glucoside pos hypothetical prote myosin heavy chain hypothetical prote probable helicase hypothetical prote 3',5'-cyclic-GMP pleishmanolysin (EC regulatory protein 3C3.20c protein conserved hypothet exopolyphosphatase uridylyltransferas nolW protein - Rhi conserved hypothet conserved hypothet RNA helicase II -Description SUMMARIES S41022 T00657 T38016 T14320 T35174 138901 A60776 SYECKP \$13032 \$30762 A53824 E69440 S61303 B25977 T31438 S05697 E72339 S34997 T22232 T40239 G64740 S04255 T10929 Length DB 311 1947 1968 829 830 918 1321 1386 853 653 415 Query Match 1 93.5 86.5 85.5 Score 81.5 81.5 81.5 81.5 81 80.5 Result

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ALIGNMENTS

RNA helicase II - human (fragments) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998 R;Valdez, B.C; Henning, D.; Busch, R.K.; Woods, K.; Flores-Rozas, H.; Hurwitz, J.; P A;Title: A nucleolar RNA helicase recognized by autoimmune antibodies from a patient A;Reference number: PC6010; MUID:96188853 A;Reference number: S72612 A;Reference number: A;Refer
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44; Gaps 58; Indels 8.4%; Score 95; DB 2; Length 200; 28.8%; Pred. No. 0.36; 24; Mismatches Conservative Query Match Best Local Similarity Matches 51, Conserv

10; 72 GVSANLP--EE--QLGALLAGMHT-----LLQQALRLPPTSLKPDT-FRDQLQELCIPQ 120 g

||:| |:|: :| :| | :| | |:|
93 VDLIGKRAAVIADAQELSQNSAIKQDAGLDIP-----EVDLVIQSSPRDVESYIHRG 145 121 -DLVGDLASVVFGSQRPLLDS-VAQQQGAWLPHVADFRWRVDVALSTS------ 167 ò g

167 ---ALARSL----QPSVLMQLKLSDGSAYRFEVPTAKFQELRYSVALVLKEMADLE 215 ö g

RESULT 2
34102

hypothetical protein T07C4.9 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C; Accession: 84102
R; Berks, M.
submitted to the EMBL Data Library, January 1994
A; Reference number: 841014
A; Reference number: 841014
A; Reference number: 841014
A; Reference number: 94102
A; Recession: 14102
A; Recession: 1676 < NBER>
A; Residues: 1-676 < NBER>
A; Residues: 1-676 < NBER>
C; Genetics:

A; Introns: 69/3; 161/1; 208/3; 227/1; 357/1; 505/3 C; Superfamily: annexin repeat homology caxis: 573-444/Domain: annexin repeat homology caxis: F; 445-516/Domain: annexin repeat homology caxis: F; 528-600/Domain: annexin repeat homology caxis

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A;Reference number: 221762
A;Accession: T38016
A;Accession: T38016
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les 42; Conserv
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R; Redecaptel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo, I. yesotskala, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, February 1998
A; Reference number: Z14197
A; Accession: T00657
A; Accession: T00657
A; Residues: Lranslated from GB/EMBL/DDBJ
A; Residues: 1-332 <FED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: AC002396; NID: 92749918; PID: 92829879; GSPDB: GN00059; ATSP: F316. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
A;Introns: 15/1; 34/3; 60/3; 86/1; 107/3; 137/3; 162/3; 173/3; 194/3; 217/3; 232/3; 265,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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C;Species: Schizosaccharomyces pombe
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38016
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F116.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVVFGSQRPLLDSVAQQQGAWLPHVADFRWRVDVAISTSAL------ARSLQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                              SLKPDIFRDQLQELCIPQDLV--GDLASVVFG------SQRPLLDSVAQQQ 145
                                                                                                                                                                                                                     146 GA-WLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRYSV 204
                                                                                                                                 43 LDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- VVSSLQGEDCR-DG 67
                                                                                                       Gaps
                                                                                                                                                        77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                     63; Indels
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                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75;
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                                                                         DB 2;
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7.6%; Score 86.5; Di
Best Local Similarity 22.2%; Pred. No. 3.7;
Matches 51; Conservative 27; Mismatches
                                                                        8.3%; Score 93.5; DE
22.7%; Pred. No. 2.2;
Live 32; Mismatches
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                           F;604-675/Domain: annexin repeat homology <AX4>
                                                                                                         Conservative
                                                                                          Similarity
41; Conserv
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                                                                             Query Match
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Matches
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Most current type: DNA
A; Most current type: DNA
A; Cross-references: EMBL: 298532; PIDN: CABI1082.1; GSPDB: GN00066; SPDB: SPACIBI.03c
A; Experimental source: strain 972h-; cosmid clBl
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 1
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calcineurin inhibitor cain - rat
calcineurin inhibitor cain - rat
calcineurin inhibitor cain - rat
calcineurin inhibitor cain - rat
calcineurin inhibitor of calcineurin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 GMHTLLQQALRLPPTSLKPDTFRDQLQELC-IPQDLVGDLASVVFGSQRPLLDSVAQQQG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    675 KILPYCDDFWTRLVQDLQSSVLDRNVKPAILSCFSDIALAIGAAFQTYLEAVWVLLQQAS 734
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                                                                                                                                                                                                                                                                                                                                                                                                               33 VAAMARLIGDLDRSTFRKLLKFVVSSLQGEDCR----DGVQRLGVSANLPEEQLGALLA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 AWLPHVADFRWRVDVAISTSALARSLQPSVL---MQLKLSDGSAYRFEV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-2182 <LAI>
A;Cross-references: EMBL:AF061947; NID:93323606; PID:93323607;
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                                                                                                                                                                                                                                                                           Length 863
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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20.8%; Pred. No. 47;
Live 34; Mismatches
                                                                                                                                                                                                                                                                     7.6%; Score 86; DB
.larity 20.9%; Pred. No. 13;
Conservative 36; Mismatches
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230k bullous pemphigoid antigen BPMI - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1993 #sequence_revision 28-May-1993
C;Accession: A60776
R;Amagai, M.; Haahimoto, T.; Tajima, S.; Inokuchi, Y.; Shimizu, N.; Saito, M.; Miki, J. Invest. Dermatol. 95, 252-259, 1990
A;Title: Partial cDNA cloning of the 230 kD mouse bullous pemphigoid antigen by use castaction: A60776; MUD:90347244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manioc,7-oxononanoate synthase (EC 2.3.1.47) - Escherichia coli
N.Alternate names: 7-KAP synthetase, 7-keto-8-amino pelargonic acid synthetase
(Species: Escherichia coli
C,Date: 30-Unn-1990 #sequence_revision 30-Jun-1990 #text_change 18-Jun-1999
C,Accession: D32025; H64813
R;Otsuka, A.J.; Buoncristiani, M.R; Howard, P.K.; Flamm, J.; Johnson, C.; Yamamoto, J. Biol. Chem. 263, 19577-19585, 198
A;Title: The Escherichia coli biotin biosynthetic enzyme sequences predicted from the A;Reference number: A32025; MUID:89066784
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                                                                                       AYGSVNKMVHKP----SG------QIMAVKRIRSTVDEKEQKQLLMDLDVVMRSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                           117 NHLKENLKIIHRDIKPSN-----ILLDRSGNIKLCDFGISGQLVDSIAKTRDAGCR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----WRVDVAISTSALARSLQP---SVLMQL------K 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 PYMAPERIDPSASROGYDVRSDVWSLGITLYELATGRFFYPKWNSVFDQLTQVVKGDPPQ 327
         3 AVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTLLQQALR--LPPTSLKPDTFRDQLQELCIPQDLV----GDLASVVFGSQRPLLDSVA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 MARLLG-DLDRSTFRKLLKFVVSSLQGE----DCRDGVQRLGVSANLPEEQLGALLAGM 89
                                                                                                                                                                                                                                            --LQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL-
                                                                                                                                                                                    ----RDG-----VQRLGVSAN-------LPEEQLGAL-LAGMHTL
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Best Local Similarity 22.4%; Pred. No. 35;
Matches 59; Conservative 30; Mismatches
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A; Residues: 1-997 <AMA>
C; Keywords: glycoprotein; membrane protein
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NAlternace names: dual specificity kinase JNKK; MAP Kinase Kinase MKK4
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 16-Peb-1996 #sequence_revision 16-Feb-1996 #text_change 18-Jun-1999
C.Date: 16-Peb-1996 #sequence_revision 16-Feb-1996 #text_change 18-Jun-1999
R.Lin, A.; Minden, A.; Martinetto, H.; Claret, F.X.; Lange-Carter, C.; Mercurio, F.; Joh
Science 268, 286-290, 1995
A.Title: Identification of a dual specificity kinase that activates the Jun kinases and A; Reference number: A56160; MUID:95232504
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A:Molecule types: mRNA
A:Molecule types: mRNA
A:Molecule types: mRNA
A:Molecule types: mRNA
A:Molecule tis uncertain whether Met-1 or Met-37 is the initiator
B:Derijard, B: Raingeaud, J: Barrett, T.; Wu, I.H.; Han, J.; Ulevitch, R.J.; Davis, F
Science 267, 682-685, 1995
A:Title: Independent human MAP kinase signal transduction pathways defined by MEK and F
A:Molecule on the contract of the
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-218 CSEDA
A; Cross-references: EMBL:AL031107; PIDN:CAA19954.1; GSPDB:GN00070; SCOEDB:SC5A7.25c
A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB:SC5A7.25c
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hypothetical protein SC5A7.25c SC5A7.25c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 VQRLGVSANLPEEQLGALLAGMHT-----LLQQALRLPPTSLKPDTFRDQLQELCIP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 QDLVG----DLASVVFGSQRPLLDSVAQQQGAWLPHVADFRWRVDVAISTSALARSLQPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphotransferase F:100-367/Domain: protein kinase homology <KIN>F:108-116/Region: protein kinase ATP-binding motif
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                                                                                                                        C. Accession: T31777 **Sequence_levision v3-Nov-1999 **Lext_change v3-Nov-1898 **Coession: T3177 **Lation v3-Nov-1999 **Lext_change v3-Nov-1998 **Le
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+1ve 22; Mismatches
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Best Local Similarity 27.11
Matches 48; Conservative
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A Molecule type: mRNA
A Residues: 37-39 CEERA
A:Cross references: GB:L36870
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Best Local Similarity
Matches 59; Conservat
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80 EQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLD 139
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nes 49; Conserv
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49; Conserv
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Best Local S:
Matches 49
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A; Mcolecule type: DNA
A; Residues: 1-384 <-075>
A; Residues: 1-384 <-075>
A; Residues: 1-384 <-075>
A; Cross-references: GB: J04423; NID: g145422; PIDN: AAA23516.1; PID: g145426
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CG
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 97426617
A; Returns: nucleic acid sequence not shown; translation not shown
A; Returns: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-384 <-BLAT>
A; Cross-references: GB: AED00180; GB: U00096; NID: g1786988; PIDN: AAC73863.1; PID: g1786993; A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
A; Gene: bloF
A; Cross-references: GB: About and Color and Color accetyltransferase homology
C; Keywords: acyltransferase: blotin blosynthesis; phosphoprotein: pyridoxal phosphate
F; 44-378/Domain: g1ycine C-acetyltransferase homology GCA>
F; 256/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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A; Residues: 1-559, R', 561-800 <BA2>
A; Cross-references: GB:X87952; EMBL:X60133; NID:g871432; PIDN:CAA61202.1; PID:g871433
A; Cross-references: GB:X87952; EMBL:X60133; NID:g871432; PIDN:CAA61202.1; PID:g871433
C; Superfamily: 3', 5'-cyclic-GMP phosphodiesterase alpha chain; 3', 5'-cyclic-nucleotide
C; Keywords: alternative splicing; cGMP binding; phosphoric diester hydrolase
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C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S:3032, S:30763
ERS Lett. 278, 107-114, 1991
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodies cing of the beta-subunit gene.
A:Reference number: S:3030; MUID:91130581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.2%; Score 81.5; DB 1; Length 384; 19.9%; Pred. No. 12; ative 32; Mismatches 90; Indels 10.
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A; Reference number: S30762
A; Accession: S30763
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A; Residues: 1-800 <BAE>
A; Cross-references: EMBL: X60133
R; Baehr, W.
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Best Local Similarity 19.99
Matches 56; Conservative
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A; Molecule type: mRNA
A; Residues: 1-2, 'X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231, 'R', 233-
A; Ross-references: EMBL: X55968; NID: 953616; PIDN: CAA39439.1; PID: 953617
A; Notes: the authors translated the codon AGA for residue 232 as Glu
c; Superfamily: 3', 5' -cyclic-GMP phosphodlesterase alpha chain; 3',5'-cyclic-nucleotid
C; Keywords: cGMP binding; phosphoric diester hydrolase
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1.559, (4,51-856 < BA2>
A; Cross-references: EMBL:X60133
R; Bowes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.
Nature: 347, 677-680, 1990
A; Title: Retinal degeneration in the rd mouse is caused by a defect in the bet.
A; Reference number: S13121; MUID:91015387
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31.5.-cycll.cGMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse
31.5.-cycll.mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 #text_change 20-Aug-1999
C;Accession: S30762; S13031; S13121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 FISEDEDVFTKYLNFATLNLKIYHLSYLHNCETRRGOVLLWSANKVFEELTDIERQFHKA 260
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                                                                                                                                                                                                                                                                                                                        80 EQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLD 139
                                                                                                                                                                                                                                           107
                                                                                 Gaps
                                                                                                                                                         32 EVAAMARLLGDLDRS----TFRKLLKFVVSSLQGEDC-----RDGVQRLGVSANLPE 79
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Submitted to the EMBL Data Library, June 1991

A. Reference number: $30762

A. Status: preliminary

A. Molecule type: mRNA

A. Molecule type: mRNA

A. Rossidues: 1-856 CARE>
A. Cross-references: EMBL:X60133; NID:953595; PIDN:CAA42719.1; PID:953596

A. Cross-references: EMBL:X60133; NID:953595; PIDN:CAA42719.1; PID:953596

A. Title: Complete cDNA sequence

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A. Title: COMP phosphoc
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Pred. No. 32;
38; Mismatches
7.2%; Score 81.5; L
19.4%; Pred. No. 30;
Live 38; Mismatches
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A; Accession: $13031
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Best Local Similarity 19.9%;
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S.Superfamily: Saccharomyces cerevisiae nuclear pore membrane protein POM152
C:Keywords: blocked amino end; duplication; glycoprotein; nuclear membrane; transmembran
F:176-195/Pomain: transmembrane #status predicted <TMM>
F:280/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A53824

A; Molecule type: DNA

A; Cross-references: GB:Z31592; NID:g473153; PID:g473154

A; Cross-references: GB:Z31592; NID:g473153; PID:g473154

A; Accession: B53824

A; Residues: 217-237; 270-302; 330-353; 417-434; 505-528; 546-563; 579-595; 684-697; 944-958; 992-89 badces: K; Achurcher, C.

B; Badcock, K; Achurcher, C.

B; Badcock, K; Achurcher, C.

B; Badcock, C; Achurcher, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclear pore membrane protein POMI52 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9553.05; protein YMR129w
C;Species: Saccharomyces cerevisiae
C;Date: 07-Oct-1994 *sequence_revision 07-Oct-1994 *text_change 24-Nov-1999
C;Accession: A53824; B53824; S53059
R;Worliak, R.W.; Blobel, G; Rout, M.P.
A;Title: POMI52 is an integral protein of the pore membrane domain of the year control of the
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
     :: || :: ---SEIVFPLDIGIVG 140
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                                                                                                                                                                                                                                                                                                                                                                                                            201 FTSEDEDVFTKYLNFATLNLKIYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQFHKA 260
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A; Molecule type: DNA
A; Residues: 1-1337 (-8AD>
A; Cross-references: EMBL:248622; NID:g728663; PID:g728668; MIPS:YMR129₩
                                                                                                                                                    SVAQ-----PSVLMQLKLSDGS-
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Query Match 7.2%; Score 81.5; Di
Best Local Similarity 25.9%; Pred. No. 56;
Matches 45; Conservative 28; Mismatches
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C;Genetics:
A;Gene: SGD:POM152
A;Gene: references: SGD:S0004736; MIPS:YMR129w
...references: Application of the control of the
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C; Accession: E69440
R; Klenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
J; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sitton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A; Reference number: A69250; MUID: 98049343
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-145 <KLE> antigen A;Cross-references: GB:AE000997; GB:AE000782; NID:92689320; PIDN:AAB89722.1; PID:9264 C;Superfamily: hypothetical protein AF1526 14; 'n, οĮ S61303
heat shock protein 63 - Neisseria meningitidis (fragment)
heat shock protein 63 - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: 27-Apr-1996 #sequence_revision 17-May-1996 #text_change 26-Aug-1999
C;Accession: S61303; S40249
Aprecession: S61303; S40249
Well Microbiol. 15, 277-285, 1995 A;Title: Construction of recombinant neisserial Hsp60 proteins and mapping A;Reference number: S61300; MUID:95264914 A;Accession: S61303 A; Status: nucleic acid sequence not shown A; Molecule type: DNA A; Residues: 1-544 PANA: A; Cross-references: EMBL: 222956; NID:g438205; PIDN:CAA80532.1; PID:g438206 C; Superfamily: chaperonin groEL C; Keywords: heat shock; stress-induced protein EELKNIAKPCDTSKEIAQVGSISAN-SDEQVGAIIAEAMEKVGKEGVITVEDGKSLENEL 187 LCIPQDLVGD-LASVVFGSQRPLLDSVAQQQGAWLPHVADFRWRV--DVAISTSALARSL 172 -----TAKFQELRYSVALVLKEMADL 214 Gaps Gaps LGAQLPPEVAAMAR-LLGD-----LDRSTFRKLLKFVVSSLQGEDCRDGVQRL---- 72 36 MARLLGDLDRS----TFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMH 90 304 EVGLFLEKATLDNIGQAKRIEIGKENTTIIDGFGDAAQIEARFAEIRQQIETATSDY-DK 18 DVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFEKKISNIRDLLPVLEKVAKASRPL 18; 91 TLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQ 144 Indels 116; ----DTFRDQLQE----Length 145; ---GVSANLPEEQLGALLA------GMHTL--40; Indels Length 84; DB 2; 3.9; ñ 21; Mismatches ; Score 81; DB ; Pred. No. 20; 45; Mismatches Score 81; Pred. No.

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hypothetical protein - Thermotoga maritima (strain MSBB)
C;Species: Thermotoga maritima
C;Stecies: Thermotoga maritima
C;Stecies: Thermotoga maritima
C;Stecies: Thermotoga maritima
C;Stecies: Tolayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C,M.
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUD:99287316
A;Reference number: A72200; MUD:99287316
A;Reference number: A72200; MUD:99287316
A;Residues: 1-161 ARNA
A;Residu
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7.1%; Score 80.5; DB 2; Length 161;
Best Local Similarity 27.7%; Pred. No. 5;
Matches 26; Conservative 20; Mismatches 35; Indels 13;
215 EKRCER 220
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363 EKLQER 368
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Search completed: May 15, 2000, 03:23:38 Job time: 5548 sec

60 QGEDCRDGVQRLGVSANL-----PEEQLGALL 86

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1 MSAVGAATP-YLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSL 59

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                                                                                           May 15, 2000, 05:34:20 ; Search time 44.1 Seconds (Without alignments) 154.692 Million cell updates/sec
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1132
1 MSAVGAATPYLHHPGDSHSG.....ALVLKEMADLEKRCERRLQD 224
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                           83857 seqs, 30454973 residues

    protein search, using sw model

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Listing first 45 summaries
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MFK_MOUSE
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CH60_NEIME
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CA36_CHICK
DYHB_CHLRE
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Q03570 caenorhabdi P5656 secherichia Q64611 rattus norv Q14494 h nuclear f P1409 cellulomona P20806 drosophila Q43593 homo sapien Q95707 homo sapien Q97192 xenopus lae Q59177 buchnera ap Q22307 caenorhabdi	SUBUNIT) (IMPORTIN 95).	L., Wood V.; bases. AND MEDIATE SERVES A RE UBUNIT (BY ENVELOPE (B' FAMILY.	the EMBI of restriction of the EMBI by and f www.isb-sib	1; Length 863; 73; Indels 50; Gaps 6; -DGVQRLGVSANLPEEQLGALLA 87
6.7 1391 1 YLDS_CAEEL 6.6 359 1 COBT_ECCLI 6.6 493 1 CSD_RAT 6.6 772 1 NFL1_HOWAN 6.6 1101 1 GUNC_CELFI 6.6 2594 1 7LES_DROVI 6.5 220 1 RP29_HUMAN 6.5 446 1 MPK2_XENLA 6.5 1301 1 DDX9_CAEEL	ALIGNMENTS TANDARD, PRT; 863 AA. 36, Careated) 36, Last sequence update) 36, Last annotation update iUBUNIT (KARYOPHERIN BETA-1 es pombe (Fission yeast). Ascomycota; Schizosaccharon	Barre o the FOR E TO ZATIC OMPLE OMPLE 3 TO 18 11	Nationalize Institute. There are no profit institutions as long as its conditions a license agreement (See http://www.mail.tolicenseeisb-sib.ch). 7. CAB11082.1; 8. CAB11082.1	7.6%; Score 86; DB 20.9%; Pred. No. 4.1 autive 36; Mismatches 36; Mismatches 37: 1.1 i.1 i.1 i.1 i.1 i.1 i.1 i.1 i.1 i.1
35 75.5 37 75.5 38 75 40 75 41 74.5 42 74 43 74 45 74	RESULT 1 1MB1_SCHPO 1 1MB1_SCHPO 21386L; 201386L; 2013886L; 2013886L; 2013886L; 20138886L; 20138886Charomyces pombe 20138886Charomyces pombe 20138886Charomyces 20138886Charom	SEQUENTIAL SUBMINISTRATION OF SU	S D T T T T T T T T T T T T T T T T T T	Ouery Match Best Local Similarity Matches 42; Conser Qy 33 VAAMARLIGDIDR; Db 580 LTSIIRREGPDIR Qy 88 GWHTILQQALRIPP Db 640 SFVPFLSSALS

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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 GMHTLLOQ------PQDLVGD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554 -ASAVHPEAYPVVAKMLAQQGISAAELIGNRERV-------KQIKASDF 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 GLNOTLAQNIVAYRDENGAEDSRKKLLKVP--RLGEKTFEQAAGFLRINGGKEPLD---- 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 OLPPEVAAMARILGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLA 87
                                                                                                                                                                                                          Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                 MEDLINE: 96236055.
Petering H., Hammerschmidt S., Frosch M., van Putten J.P.M., Petering H., Hammerschmidt S., Frosch M., van Putten J.P.M., Ison C.A., Robertson B.D., "Genes associated with meningococcal capsule complex are also found "Genes associated with meningococcal capsule complex are also found
                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%; Score 85.5; DB 1; Length 757;
illarity 23.2%; Pred. No. 3.9; 68; Indels 6:
Conservative 27; Mismatches 68; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 AA; 83064 MW; EAAF4D9A8197C944 CRC64;
           147 AWLPHVADFRWRVDVAISTSALARSLOPSVL---MOLKLSDGSAYRFEV---
                                                                                                                                                                                                                                                                                                                      2182 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 83.1 KD PROTEIN IN REGION E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 SAYRFEVPTAKFQELRYSVALVLKEMADLEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595 IDERFGLPT------ILDILSELEK 613
                                                                                                                                               757 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L09189; AAC37046.1; -.
HSSP; P05055; 1SRO.
                                                                 193 ----PTAKFOELRYSVALVL 208
                                                                                       735 SVQAPPGANFSMIDYVDALRL 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                    STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
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                                                                                                                                                      YHGF_NEIME
Q51152;
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Sanchez I., Hughes R.T., Mayer B.J., Yee K., Woodgett J.R., Avruch J., Kyriakis J.M., Zon L.I.; in the stress-activated pathway regulating Ryriakis J.M., Zon I.I.; in the stress-activated pathway regulating Franscription factor C.Jun.";
Nature 372:794-798(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2010 (Rel. 39, Last Annotation update)
16-C 2. 7. 1. 9) (MAP KINASE KINASE 4) (MAPKK 4) (MAPKK/FRK KINASE 1)
ACHIVATING KINASE 1) (C-UN N-TERMINAL KINASE 1) (JNK KINASE 1)
ACHIVATING KINASE 1) (SEK.).
(JNKK 1) (SAPK/FRK KINASE 1) (SEK.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1293 EAAEGPFARGEEKNTPKASEKEKACLVDEDSHSSAGTLPGPGASLPSSSGPGLTSPPYTA 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1236 YLHEEAARYPKKIHY---HNPPELAMEALEVYFRLHASILKLIGKPDSGVSAEVLVSFMK 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 L-------QQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPL-- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 98325042.
MEDLINE; 98325042.
Lai M.M. Burnett P.E., Wolosker H., Blackshaw S., Snyder S.H.;
"Cain, a novel physiologic protein inhibitor of calcineurin.";
"Cain, a novel physiologic protein inhibitor of calcineurin.";
"Cain, a novel physiologic protein inhibitor of calcineurin.";
J. Blol. Chem. 273:18325-18331(1998).
J. FULL Chem. 273:18325-18331(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 YLHHPGDSHSGRVSFLGAQLPPEV-----AAMARLLGDLDRSTFRK-LLKFVV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 ----LDSVAQQQAMLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAY 188
                    (CAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 2182;
                                               Rattus norvogicus (Rat).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
15-FEB-2000 (Rel. 39, Last annotation update)
CALCINEURIN-BINDING PROTEIN CABIN 1 (CALCINEURIN INHIBITOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF061947; AAC40176.1; -. S904C335AB3F440A CRC64; SEQUENCE 2182 AA; 242811 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.6%; Score 85.5; DE
Local Similarity 20.8%; Pred. No. 14;
hes 49; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Eutheria; Primates; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        Murine cytomegalovirus (strain Smith).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                            Helicase; DNA
SEQUENCE 961
                                                                                                                                                                                                                                                                                                                                                                                                                                         802 LESGOS 807
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Best Local S
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P45985
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MPK4_HUMAN
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                                                                                                                                                                                   13;
           niffed (DEC-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: DUAL SPECIFICITY KINASE THAT ACTIVATES THE JUN KINASES
MAPKI (ERK2) OR MAPK3 (ERK1). AS WELL AS MAPK14 (F38) BUT NOT
                                   MAPKI (ERKZ) OR MAPK3 (ERKI).

-!- PIM: ACTIVATED BY PHOSHORYLATION ON SER/THR BY MAP KINASE KINASE
                                                                                                                                                                                          MGD; MGI-107199; SERKI.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PRAM; PRO0069; PKINASE, 1.
PRAM; PRO0069; PKINASE, 1.
PRAM; PRO0069; PKINASE, 1.
APP-binding; Phosphorylation.
APP-binding; Phosphorylation.
                                                                     BRAIN AND MUSCLE.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                     3 AVGAATPYLHHPGDSHSGRVSFLGAOLPPEVAAMAKLLGDLDRSTFRKLLKFVVSSLQGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                          155 CPYIVQFYGALFREGDCWICMELMSTSFDKFYKXVYSVLDDVIPEBILGKITLATVKAL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                            93 --LOQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWL- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 PHVADER-----WRVDVAISTSALARSLQP---SVLMQL-----K 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: IS EXPRESSED ABUNDANTLY IN THE ADULT
                                                                                                                                                                                                                                                                                                                 ->R: LOSS OF ATP-BINDING ACTIVITY.
B99C6688184E5B3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UL70, MCMVS STANDARD; PRT; 964 AA.
UL70, MCMVS (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HELICASE/PRIMASE COMPLEX PROTEIN (PROBABLE DNA REPLICATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 LSNSEEREFSPSFINFVNLCLTKDESKRPKYKELLKHPFILMYEERTVEVAC 377
                                                                                                                                                                                                                                                                                                                                              7.3%; Score 83; DB 1; Length 397;
20.2%; Pred. No. 2.9;
tive 44; Mismatches 89; Indels
                                                                                                                                                                                                                                                                    GLY/SER-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY).
K->R: LOSS OF ATP-BIND
                                                                                                                                                                                                                                                                     100 366 PRO
103 111 ATP
227 227 227 BY
129 129 ATP
397 AA, 44113 MW, E
                                                                                                                                                                            EMBL; U18310; AAB81554.1; HSSP; P00518; 1PHK
                                                                                                                                                                                                                                                                                                                                                 Similarity 20.2°
59; Conservative
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Local Sim
59;
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BINDING
ACT_SITE
MUTAGEN
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                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
RESULT 5
UL70_MCMVS
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REPORTINE; 96082764.

RAY MEDLINE; 96082764.

RAY MEDLINE; 96082764.

RAY Characterization of a conserved gene block in the murine cytomegalovirus genome. "

Cytomegalovirus genome."

RIC STRICARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52.

"INITARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52.

"EHV-1 7. EBV BSLF1, HVS-1 56, V2V 6, HCWA NDD MCMV UL70.

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CC The European Bioliformatics Institute. There are no restrictions on its content is not removed. Since content is in no way contined and this statement is not removed. Usage by and for commercial content (Seen thep://www.isb-sib.ch/announce/ 641 PPRTAAIGAQTLKRLAGILDHTLCLDRDLVCKLNAISHPGECFDTGIYSHGRSIRWPLMY 700 79 --EEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQ-----LQELCIPQDLVGDLASVVF 131 30 PPEVAA-----MARLLGDLDRSTF--RKLL-KFVVSSLQGEDCRDGVQRLGVSANLP--- 79 701 KLDEASGLIL---HS-----RLNPIFIVPAGYRDRPAEFVLOOLG-PQNL-----TH 743 132 GSQRPLLDSVAQQQGAWLPHVAD------FRWRVDVAISTSALARSLQPSVLMQLK 181 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-FEB-200 (Rel. 39, Last sequence update)
05-A. SPECIFICITY MITOGEN-ACTIVATED PROTEIN WIDSTED
(EC 2.7.1.) (MAP KINASE KINASE 4) (JUNK ACTIVATING KINASE 4
MAP2R4 OF PREMIT OF MIXIS (SAPK/SFR KINASE 1) (C-JUN N-SEQUENCE: FROM N.A.
MEDLINE; 95232504.
Lin A., Winden A., Martinetto H., Claret F.-X., Lange-Carter C.,
Mercurio F. Johnson G.L., Karin M.;
Kinases and p38-Mpk2.";
Science 268:286-290(1995). ch 1 Similarity 7.3%; Score 82.5; DB 1; Length 964; 51; Conservative 1 21; Mismatches 67; Indels 4; NA replication. 964 AA; 109704 MW; 70605300E1D85864 CRC64; [2] SEQUENCE FROM N.A TISSUE-BRAIN,

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"The complete genome sequence of Escherichia coll K-12.";
Schence 277:453-1474(1997).
-1. CATALYTIC ACTIVITY: 6-CARBOXHEXANOYL-COA + L-ALANINE -
8-AMINO'7-CANONANATE + COA + CO(2).
-1. COFACTOR: PYRIDOXAL PHOSPHATE.
-1. COFACTOR: PYRIDOXAL PHOSPHATE.
-1. PATHWAY: BIOTIN BIOSYNTHESIS PATHWAY.
-1. SIMILARIY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-K12 / MG1655;

STRAIN-K12 / MG1655;

MEDLINE: 9742661.

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Mayhew G.F.,

Blattner F.R., Plunkett G. III, Bloch C.K., Mayhew G.F.,

Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K.,

Rode C.K., Mayhew G.F.,

Rango J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

Gregor J., Davis N.W., Kirkpatrick H.A.,

Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 137, Last annotation update)
8-AMINO-7-OXONORNOATE SYNTHESE (EC 2.3.1.47) (7-KETO-8-AMINE-PIMELYL COA
PELARGONIC ACID SYNTHETASE) (7-KAP SYNTHETASE) (L-ALANINE--PIMELYL COA
LIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Otsuka A.J., Uchida K., Cuok C., Ruppert J., Matsuzaki J., Johnson O., yamamoto R., Uchida K., Cuok C., Ruppert J., Matsuzaki J., Yamamoto R., Cuokida K., Cuok C., Ruppert J., Matsuzaki J., The mandot R., Chotin biostrintetic enzyma sequences predicted from the nucleotide sequence of the bio operon.";

From the nucleotide sequence of the bio operon.";
J., Biol. Chem. 263:19577-19585(1988).
                                                                                                                        150 PHVADER----K 181
                                                                                                                                                                                     268 PYKAPERIDPSASRQGYDVRSDVWSLGITLYELAIGREPYPKWNSVFDQLIQVVKGDPPQ 327
93 --LAGALRLPPTSLKPDTERDQLQELCIPQDLVGDLASVVFGSGRPLLDSVAQQGGAWL- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. P.A.; Pearson of biotin synthetase enzymes."; Pearson B.M., McKee R.A.; "Genetic material for expression of biotin agential for expression 11-ocr-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                               217 NHLKENLKIIHRDIKPSN-----ILLDRSGNIKLCDFGISGQLVDSIAKTRDAGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; D32025; SYECKP.
ECOGENE: EG1021; BIOF.
ECOGENE: PS00592; AA_TRANSFER_CLASS_2; 1.
PROSITE: PS00522; aminotran_2; 1.
PFAM: PF00222; aminotran_2; 1.
Biotin blosynthesis; Transferase; pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                     328 LSNSEEREFSPSFINFVNLCLTKDESKRPKYKELLKHPFILMYEERAVEVAC 379
                                                                                                                                                                                                                                                                   182 LSDGSAYRF-----EVPTAKFQELRYSVALVLKEMADLEKRC
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EMBL; All542; CAA00968.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation its between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DC-----RDG----VQRLGVSAN------LPEEQLGAL-LAGMHTL 92
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PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00069; PKinase; 1.
Iransferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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TALETATIONS IN PANCEALLC, DILLARY, and breast carcinomas support

RT MKK4 as a genetically targeted tumor suppressor gene.";

RT MKK4 as a genetically targeted tumor suppressor gene.";

RT CANCE STATE STATE OF MAPPERSORY

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THE SECTION OF S
                                                                                                                                                        Derijard B., Raingeaud J., Barrett T., Wu I.-H., Han J.,
Derijard B.J., Davis R.J.;
Ulevitch R.J., Davis R.J.;
Ulevitch R.J., Davis R.J.;
"Independent human MAP-kinase signal transduction pathways defined by
"Independent human MAP-kinase";
"Independent human MAP-kinase signal transduction pathways defined by
"Independent human MAP-kinase";
"Independent human MAP-kinase signal transduction pathways defined by
"Independent human MAP-kinase";
"Independent human MAP-kinase signal transduction pathways defined by
"Independent human MAP-kinase";
"Independent human MAP-kinase signal transduction pathways defined by
"Independent human MAP-kinase";
"Independent human MAP-kinase signal transduction pathways defined by
"Independent human MAP-kinase";

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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE: 98283389.
Su G. H., Hilgers W., Shekher M.C., Tang D.J., Yeo C.J., Hruban R.H.
Kern S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 82; DB 1; Length 399;
20.2%; Pred. No. 3.6; 89; Indels :
ive 44; Mismatches 89; Indels :
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
W; A472537F2F26770B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L. AFO70080; AAC24130.1; JOINED. L. AFO70080; AAC24130.1; JOINED. L. AFO70081; AAC24130.1; JOINED. L. AFO70083; AAC24130.1; JOINED. L. AFO70084; AAC24130.1; JOINED. L. AFO70085; AAC24130.1; JOINED. L. AFO70086; AAC24130.1; JOINED. L. AFO70088; AAC24130.1; JOINED. L. AFO70089; AACZ4130.1; JOINED. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44287 MW;
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port Local Similarity
Matches 59; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                  99 YSRALLFISGFAANQAVIAAMMAKEDRIAADRLS-------HASILEAAS 141
                                                                                                                                                                                                                                                                                    99 LPPTSLKPDTFRD-----QLQELCIPQDLVGDLASVVF---GSQRPL--LDSVAQQQGA 147
                                                                                                                                                                                                                                                                                                                    142 LSPSOLRRFAHNDVTHLARLLASPCPGQOMV--VTEGVFSMDGDSAPLAEIQOVTQOHNG 199
                                                                                                                                                                                                                                                                                                                                                                                    200 WL-----MVDDAHGTGVIGEQGRGSCWLQKVKPELLVVTFGKGFGVSGAAVLCSSTV 251
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SUCH AS
                                                                                                                              Gaps
                                                                                                                                                   6 AATPYL---HHP------GDSHSGRVSFLGAQLPPEVAAMARLLGDLDRST 47
                                                                                                                                                                                              66
                                                                                                                                                                                                                   48 FRKLLKF------VVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (MAR-1995) to the EMBL/GenBank/DbBJ databases.
-!-FUNCTION: COMPONENT OF THE NUCLEAR PORE COMPLEX WHICH MAY PROVID
THE NECESSARY SAYMETRY REQUIRED FOR ANGIORING STRUCTURES SUCH A
CYTOPLAAMIC FILAMENTS AND THE NUCLEOPLANIC CAGE.
-!- SUBGUNIT: INTERACTS WITH NUP170 AND/OR NUP188.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. NUCLEAR PORE
                                                                                                                                                                                  45 SSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POM152 OR YMR129W OR YM9553.05.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi: Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wozniak R.W., Blobel G., Rout M.P., "POM152 is an integral protein of the pore membrane domain of the yeast nuclear envelope.";
J. Cell Biol. 125:31-42(1994).
                                                                                                                         90; Indels 103;
     PYRIDOXAL PHOSPHATE (PROBABLE).
                                                                                          DB 1; Length 384;
                   AE -> R (IN REF. 2).
D1AF5C054A5B4B06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (P150).
                                                                                                                                                                                                                                                                                                                                                    148 WLPHVADFRWRVDVAISTSALA-----RSLQPSVLM----
                                                                                                                                                                                                                                                                                                                                                                                                                      179 ---QLKLSDGSAYRFEVPTAKFQELRYSVALVLKEMADLEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POMIS2
                                                                                       Score 81.5; Di
Pred. No. 3.8;
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI; 1337 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE.
-!- PTM: THE N-TERMINUS IS BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetaceae; Saccharomyces
                                     41594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 31, Created)
                                                                                     7.2%;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
 236
188
384 AA;
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=W303;
MEDLINE; 94186543
                                                                                 Query Match
Best Local Simi
Matches 56;
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P152_YEAST
P39685;
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BINDING
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                            VSSLQGEDCRDGVQRLGVSANLPEEQLGA---LLAGMHTLLQQALRLPPTSLKPDTFRDQ 112
                                                                                                                                                                                                                                                                                                                                               438 LOSSKSKOSFTQGELNDLKWGRNOPVNINLDSSITQDG-----KFAYKIDKI--TDGL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. MICTODIOL. 15:277-285(1995).
-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
-1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC AND LOOSELY ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pannekoek Y., Dankert J., van Putten J.P.M.;
"Construction of recombinant neisserial Hsp60 proteins and mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                   113 LQELCIPQDLV-GDLASVVFGSQRPL---LDSVAQQQGAWLPHVADFRWRVDVAISTSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           169 ARSLQ-PSVLMQLKLSDGSAYRF---EVPTAKFQE-----LRYSVALVLKEM 211
                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (63 KD STRESS
                                                                                                                                                                                                                                                                             Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 GNVVDFTSLPEELKKRYDLSYNFNVHEVPRAALEERFDPKSPTKRSIAIVFEEI
                                                                                                    8 X 24 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                         Indels
                                                      POTENTIAL.
CISTERNAL SIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUTER MEMBRANE.
                                                                                                                                                                                                                                 A024A42069193898 CRC64;
                               e; Repeat; Glycoprotein.
PORE SIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                         Score 81.5; D
Pred. No. 18;
28; Mismatches
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                               Transmembrane;
                                                                                                                                                                                                                                MM;
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(Rel. 32, Last sequ
(Rel. 39, Last anno
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN) (GSP63).
MOPA OR GROEL OR HSP63.
PIR; A53824; A53824.
SGD; L0001464; POM152.
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Thes 45; Conservat
                                                                                                                                                                                                                                A);
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                         Nuclear protein;
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P42385;
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                                                                    DOMAIN
CARBOHYD
                                                        TRANSMEM
                                                                                                                                                                                                                             SEQUENCE
                                        DOMAIN
                                                                                                  DOMAIN
                                                                                                              REPEAT
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CH60_NEIME
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EMBL; Z31592; CAA83469.1; -. EMBL; Z48622; CAA88554.1; -.

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                                                                                                                                                                                                                                                                                            14;
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Expression of the ferric enterobactin receptor (PfeA) of Pseudomonas "Expression of the ferric enterobactin receptor (PfeA) of Pseudomonas aeruginosa: involvement of a two-component regulatory system.";
Mol. Microbiol. 8:1095-1103(1993).
-!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PFER/PFES.
-!- FUNCTION: MARS ACTIVATE PPER BY PHOSPHORYLATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 EVGLFLERATLDNLGQAKRIEIGKENTTIIDGFGDAAQIEARFAEIRQQIETATSDY-DK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCIPQDLVGD-LASVVFGSQRPLLDSVAQQQGAWLPHVADFRWRV--DVAISTSALARSL 172
                                                                                                                                                                                                                                                                                                                                                                   :||; ||; ||; ||; || ||; || ||; || ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 EELKNIAKPCDTSKEIAQVGSISAN-SDEQVGAIIAEAMEKVGKEGVITVEDGKSLENEL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
KINASES.
                                                                                                                                                                                                                                                                                                                                       25 LGAQLPPEVAAMAR-LLGD-----LDRSTFRKLLKFVVSSLQGEDCRDGVQRL---- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TAKFQELRYSVALVLKEMADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVVEGMOFDRGYLSPYFINDAEKQIAGLDNPFVLLFEKKISNIRDLLPVLEKVAKASRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                              84; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GVSANLPEEQLGALLA------GMHTL-----
                                                                                                                                                                                                                                             7.2%; Score 81; DB 1; Length 544;
19.9%; Pred. No. 6.5;
tive 45; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LOGALRIPPISIKP-------DIFRDQLQE---
                                                                                                                                                                           B0789DA091149D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                            HSSP; PO6139; IGRL.
PRINTS; PR00298; CHAPERONINGO.
PROSITE; PR00296; CHAPERONINS_CPN60; 1.
PROSITE; PS00296; CHAPERONINS_CPN60; 1.
PFAM; PF00118; cpn60_TCP1; 1.
Chaperone; ATP-binding; Antigen.
SEQUENCE 544 AA; 57580 WW; B0789DAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
sensor protein PFES (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 QPSVLMQLKLSD--GSAYRFEVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
       EMBL; 222956; CAA80532.1;
                                                                                                                                                                                                                                                     0uery Match
Best Local Similarity 19.9
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PAO;
MEDLINE; 93368425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 EKRCER 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 EKLQER 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFES_PSEAE
Q04804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFES_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
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319 SGWDPARLPCRLGVDCRV-EVHLDSLAQAMENLLRNAIRHSPEDGTVSLDGEREGDFWHL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                   27 AQLPP-----EVAAMARLLGD-LDRS-----TFRKLLKFVVSSLQGEDCRD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; Burland V.D., and analysis of 136 kilobases of the Escherichia coll genome: organizational symmetry around the origin of replication."; Genomics. 16:551-561(1993).
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Ш
                                                                                                                                                                                                                                                                                                                                                                                 nucleotide
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Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 87222180.
Schnetz K., Toloczyki C., Rak B.;
"Beter glucoside (bgl) operon of Escherichia coli K-12: nucleoti
"Beter glucoside (bgl) operon of Escherichia evolutionary
sequence, genetic organization, and possible evolutionary
relationship to regulatory components of two Bacillus subtilis
                                                                                                                                                                                                                                                                                                                  62; Indels | 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahadevan S., Wright A.;
Mahadevan S., Wright A.;
Ma bacterial gene involved in transcription antitermination:
regulation at a rho-independent terminator in the bgl operon
                                                                                                                                                                                                                                                                    DB 1; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                     67 G-----VQRLGVSANLPEEQLGALLAGMHTLLQQALRLPP----TSLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PDIFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGA-----
                                                        Sensory transduction; Transferase; Kinase; Phosphorylation
Transmembrane; Inner membrane.
                                                                                                                                                                                              (BY
                                                                                                                                                                                              PHOSPHORYLATION (AUTO-) (62B78FED184FE73E CRC64;
                                                                                                                                                         POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                  PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-00T-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35) Last annotation update)
CRYPIC BETA-GLUCOSIDE BGL OPERON ANTITERMINATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŕ
                                                                                                                                                                                                                                                                          7.1%; Score 80.5; DE 24.3%; Pred. No. 5.6; ative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 169:2579-2590(1987).
                                                                                                                                                                                                                     MM;
EMBL; L07739; AAA25930.1; -. PFAM; PF00512; signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-197 FROM N.A.
                                                                                                                                                                                                                     50597
                    PF00512; signal; 1. PF00672; DUF5; 1.
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                   30
155
176
246
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STRAIN-K12 / MG1655;
MEDLINE; 93315143.
                                                                                                                                        31
156
177
244
446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 87273510.
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 LHLWLPAAA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---WLPHVA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BGLG OR BGLC.
                                                                                                                                                                                                                                                                                    Ma.
Local Sim.
46;
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P11989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K12;
                                                                                                                                                           TRANSMEM
DOMAIN
MOD_RES
SEQUENCE
                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes.
                                                                                                      DOMAIN
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
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                                         PFAM;
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PIR; S05697; S05697.
HSSP: P08799; 1MND:
PFAM; PF00063; myosin_head; 1.
PFAM; PF01576; myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>.
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w
                                                                                                                                                                                                                                                                    HOLDMAN F., DIAZ-TOTE M.R., WRIGHT A.;

"Transcriptional antitermination in the bgl operon of E. coli is modulated by a specific RNA binding protein.";

cell 67:1153-1163(1990).

-: FUNCTION: MEDIATES THE POSITIVE REGULATION OF THE BETA-GLUCOSIDE (BGL) OPERON BY FUNCTIONING AS A TRANSCRIPTIONAL ANTITERMINATOR.

THIS IS A RNA-BINDING PROTEIN THAT RECOGNIZES A SPECIFIC SEQUENCE LOCATED JUST UPSTREAM OF TWO TERMINATION SITES WITHIN THE OPERON.

-: PTW. PHOSPHORYLATED AND INACTIVATED BY BGLF (II-BGL). THE DEGREE OF PHOSPHORYLATED AND INACTIVATED BY BGLF (II-BGL). THE DEGREE OF PHOSPHORYLATED SHICK ASSENCE OF BETA-GLUCOSIDES WHICH ACT AS INDUCERS OF THE OPERON EXPRESSION.

ADDITION OF INDUCER RESULT IN THE RAPID DEPHOSPHORYLATION OF BGLG.

-: SAUMLARAITY: BELONGS TO THE TRANSCRIPTIONAL ANTITERMINATOR BGLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 ANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIPQDLYGDLASVVFGSQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 ------RPLL-----BSVAQQGGWLPHVADFRWRVDVAISTS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 MSGNMEDVAGVTQLMREMLQLIKFQFSLNYQEESLSYQR--LVTHLKFLSWRILEHASIN 223
                                                                                                                                      Schnetz K., Rak B.;
Schnetz K., Rak B.;
"Beta-glucoside permease represses the bgl operon of Escherichia col
by phosphorylation of the antiterminator protein and also interacts
with glucose-specific enzyme III, the key element in catabolite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 SH--SGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Gaps
                                                                                  œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation.
                                                             Amster-Choder O., Wright A.; "Regulation of activity of a transcriptional anti-terminator in coli by phosphorylation in vivo."; Science 249:540-542(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00874; Bg1G_antitermin; 2.
Transcription regulation; Activator; RNA-binding; Phos
SEQUENCE 278 AA; 32097 MW; 5ACF1A14BF438B4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 3.5; 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECGENE; EG10116; BGLG.
PROSITE; PS00654; ANTITERMINATORS_BGLG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 80;
21.8%; Pred. No.
                                      REGULATION BY PHOSPHORYLATION. MEDLINE; 90341774.
                                                                                                                              REGULATION BY PHOSPHORYLATION. MEDLINE; 90311345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M16487; AAA23509.1; -.
EMBL; L10328; AAA62074.1; -.
EMBL; AE000449; AAC76746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M17098; AAA23512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
coli.";
Cell 50:485-494(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A27161; A27161.
PIR; B25977; B25977.
HSSP; P15401; 1AUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                              90381772.
                                                                                                                                                                                                                                                 RNA-BINDING
MEDLINE: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: THE GLOBULAR HEAD AA SEQUENCE SHOWS A HIGH DEGREE OF SIMILARITY WITH THE GLOBULAR HEAD SEQUENCES OF WUSCLE & NONWUSCLE HEAVY CHAINS. BY CONTRAST THE ROD SEQUENCE IS LESS CONSERVED, BUT THE PRRIODICITIES OF HYDROPHOBIC & CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE, ARE CONSERVED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C.
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dibb N.J., Maruyama I.N., Krause M., Karn J.; "Sequence analysis of the complete Caenorhabditis elegans myosin
     --QLKLSDGSAYRFEVPTAKFQELRYSVALVLKE 210
                                        224 DSDESLQQAVKQNYPQAWQCAERIAIFIGLQYQRKISPAEIMFLAINIERVRKE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-21; 112-371 AND 1501-1772 FROM N.A.
                                                                                                                                                                                                                               01-ocT-1989 (Rel. 12, Created)
01-ocT-1989 (Rel. 12, Last sequence update)
12-UL-1998 (Rel. 36, Last annotation update)
MYOSIN HEAVY CHAIN C (MMC C).
                                                                                                                                                                                      1947 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Mol. Biol. 205:603-613(1989).
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EMBL; M37235; AAA28122.1;
EMBL; M37236; AAA28123.1;
                                                                                                                                                                                    STANDARD;
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167 ALARSLOPSVLM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 89178677.
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NAMES OF STREET 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKGFPNRTLHPDFVQRYALLAADESIIGKTDAKKGSALMLARLVKEKKLEEENFRVGLTK 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASV-----VFGSQRPLLDS--VAQQQGAWLPHVADFRWRVDVAISTSALARSLQ---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 838 AELRIWWFKLYGKVKPLVNSGKIEAQYEKLQETVATLK---DTVVQEEEKKRQLQEGAE 894
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STRAIN=K12 ' W3110;
STRAIN=K12 ' W3110;
where y 4018640.
van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.;
"The genes of the glutamine synthetase adenylylation cascade are not
regulated by nitrogen in Escherichia coli.";
Mol. Microbiol. 9:443-458(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVSFLGAQLPPE-----VAAMARLLG--DLDRSTFRKLLKFV-VSSLQGEDCRDGVQR 70
in, Muscle protein, Colled coil; Thick filament, Actin-binding; binding; Methylation; Alkylation; Heptad repeat pattern;
                                                                                                      COLLED COLL (FORENTIAL).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
ACTIN-BINDING.
ALKYLATION (SH-1).
E -> D (IN REF. 2).
E -> I (IN REF. 2).
M-> I (IN REF. 2).
M-> I (IN REF. 2).
M-> I (IN REF. 2).
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Escherichia.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 29, Last annotation update)
11-PROTEIN-PII] URIDYLYLTRANSFERASE (EC 2.7.7.59) (PII URIDYLYL-
TRANSFERASE) (URIDYLYL REMOVING ENZYME) (UTASE).
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Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                       GLOBULAR HEAD (S1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.1%; Score 80; DB
22.2%; Pred. No. 39;
ive 41; Mismatches
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STAIN-MLZ / W3110;
MEDLINE; 9426430.
Fujita N., Mori H., Yura T., Ishihama A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local Similarity 22.2
Matches 57; Conservative
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                                                            Multigene family.
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MOD_RES
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-1- SIMILARITY: TO OTHER BACTERIAL GLND.
-1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 703
-1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 703
-1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 703
-1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PII
                                                                                                        SEQUENCE FROM N.A.
STRAIN-KI2 / MGIG55;
MEDLINE; 97426617.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Maybew G.F., Riley M., Chi and W., Kirkpatrick H.A., Goeden M.A., Rose, D.J., Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MODIFIES, BY URIDYLYLATION OR DEURIDYLYLATION THE
(GLMB) REGULATORY PROTEIN.
-!- CATALYTIC ACTIVITY: UTP + [PROTEIN-PII] - PYROPHOSPHATE +
        analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                 Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chun
Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 890;
                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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G -> A (IN REF. 3).

RG -> TR (IN REF. 1).

D -> H (IN REF. 1).

A -> R (IN REF. 2).

A -> R (IN REF. 2).
"Systematic sequencing of the Escherichia coli genome:
the 2.4-4.1 min (110,917-193,643 bp) region.";
Nucleic Acids Res. 22:1637-1639(1994).
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EMBL, 221842; CAA79887.1; --
EMBL, D26562; CAB20283.1; ALT_FRAME.
EMBL, AE000126; AAC73278.1; --
EMBL; J70214; AAB08596.1; --
PIR, S31962; S31962.
FIR, S36284, S36284.
ECGENE; EG11411; GLND.
CONFLICT
47 % L --> S (I)
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7890 AA;
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Best Local Simi
Matches 56;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quinate metabolism; Transcription regulation; Repressor; DNA-binding.
SEQUENCE 918 AA; 100580 MW; 67EDA399CBF098B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 SHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSAN 76
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                             Geever R.F., Huiet L., Baum J.A., Tyler B.M., Patel V.B., Rutledge B.J., Case M.E., Giles N.H.; "DNA sequence, organization and regulation of the qa gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 LPEEQL--GALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOY-1991 (Rel. 20, Created)
01-NOY-1991 (Rel. 20, Last sequence update)
11-JUL-1998 (Rel. 36, Last annotation update)
ROD GGMP-SPECIFIC 3', CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT
(EC 3.1.4.17) (GMP-PDE BETA).
BDEGB OR PDEB.
BOS taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Peccoa; Bovoidea; Bovidee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 SESGPTSPLGL-APHRASEISRVVGEIRRDTVIPIILHVV--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 918;
                                                                                                                                                                                                                                                               J. Mol. Biol. 207:15-34(1989).
-!- FUNCTION: REPRESSOR FOR ENZYMES AND PROTEINS OF QUINATE
                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pyrenomycetes; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                          01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
0UINATE REPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.0%; Score 79.5; DB Best Local Similarity 27.0%; Pred. No. 17; Matches 40; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 VFGSQRPLLDSVAQQQGAWLPHVADFRW 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 VIGNKQ-----LAEVNSPRW 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF01487; DHquinase_I; 1. PFAM; PF01488; Shikimate_DH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X14603; CAA32753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                  STANDARD;
                                                                                                            QA-1S.
Neurospora crassa.
Eukaryota; Fungi; 1
                                                                                                                                                                       SEQUENCÉ FROM N.A.
STRAIN-74-OR23-1A;
MEDLINE; 89293848.
                                                                                                                                                                                                                                                      Neurospora crassa.
                                                                                                                                                                                                                                                                                           METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Cet
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNRB_BOVIN
P23439;
                                  QA1S_NEUCR
P11637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNRB_BOVIN
                      QA1S_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 DSVAQ-----QQGAWLPHVADFRWRVDVAISTSALARSLQ-----PSVLMQLKLSDGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; CGMP; Vision; Prenylation; Lipoprotein; Membrane.

CHAIN

1 850 ROD CGMP-SPECIFIC 3',5'-CYCLIC
PROPEP 851 853 REMOVED IN MATURE FORM (BY SIMILARITY).

CONFLICT 483 484 DE -> EQ (IN REF. 2).

SEQUENCE 853 AA; 98330 MW; C4B3F22CFFE7F2FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 EVAAMARLLGD-----LDRSTFRKLLKFVVSSLQGEDC-----RDGVQRLGVSANLP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIOCOG. Khim. 16:118-120(1990).
-!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF TANNSMISSION AND AMPLETCATION OF THE VISUAL SIGNAL. NECESSARY FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOGNIXME.
-!- CATALYTIC ACTIVITY: GUANOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O = GUANOSINE 5'-PHOSPHATE.
-!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 -------AYRFEVPTAKFQELRYSVALVLKEMADLEKR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 ------SEIVFPLDIGVV
                                                                                                                                                                                        Applebury M.L.;
Beta-subunit of bovine rod photoreceptor cGMP phosphodiesterase.
Comparison with the phosphodiesterase family.";
J. Biol. Chem. 265:12955-12959(1990).
                                                                                                           Lipkin V.M., Khramtsov N.V., Vasilevskaya I.A., Atabekova N.V., Muradov K.G., Gubanov V.V., Li T., Johnston J.P., Volpp K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90267525.
Lipkin V.M., Gubanov V.V., Khramtsov N.V., Vasilevskaya I.A., Atabakova N.V., Muradov K.G., Shuvaeva T.M., Surina E.A., Zagranichny V.E., Li T., H. T., R. Surina E.A., "Cyclic GMP phosphodiestel hase from bovine retina. Amino acid se of beta-subunit and nucleotide sequence of corresponding cDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 79; DB 1; Length 853; 20.7%; Pred. No. 17; ive 36; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00387; PDIESTERASE1.
PROSITE; PS00126; PDEASE_1; 1.
PFAM; PF00037; fer4; 1.
PFAM; PF00233; PDEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, J05553; AAA30440.1; -. EMBL; X57146; CAA40436.1; -. PIR; A36617; A36617. PIR; S19145; S19145.
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Matches 49; Conservative
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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200 CFTSEDEDVFLKYLNFGTLNLKIYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQ 256 q

Search completed: May 15, 2000, 05:34:23 Job time: 12493 sec

Page 10

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051812 mygus persi
094235 schizosacch
096336 drosophila
023326 caenorhabdi
066002 california
066003 california
066003 california
09547 azospirillu
09547 azospirillu
094439 bacillu
032441 pseudomonas
08684 streptomyce
032444 drosophila
044708 drosophila
                                                                                                                                                                                                                                                                                                                                                                       P95022 mycobacteri
006264 mycobacteri
09ye72 aeropyrum p
030854 vibrio chol
                                                                                                                                                                                                                                                                                                                     09zln3 rattus norv
09x8v6 streptomyce
P89467 herpes simp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 PVVLKHCHAAAATCILEAGHMQVDKSTLSTYLEDCKFDRERI-ELFCTEYQNNKNSLETL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AQQGAWLPHVADFRWRVDVAĮSTSALARSLQPSVLMQLKL--SDGSAY---RFEVPTAK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 LGSIGRSLPHITDVSWRLEYQIKTNOLHKMYRPGYLVTLNVENNDSQSYPEINFSCNMEQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 93165034.
HAUPT Y., BARRI G., ADAMS J.M.;
"Nucleotide sequence of bup, an upstream gene in the bmi-1 proviral insertion locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GSFDSNAFALLLRAAFQSL-----LDARADEAALD-----HPYLKQ---ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5%; Score 96; DB 11; Length 195; 20.8%; Pred. No. 0.2; tive 32; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
BUP-5'OF BMI-1 PROVIRAL INSERTION LOCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOI. Biol. Rep. 17:17-20(1992).
EMBL: S54914; AAB25378.1; -.
MGD; MGI:88218; Bup.
SEQUENCE 195 AA; 22037 MW; 827A84F1 CRC32;
                                                                                                                                                                                          Q9X838
Q53730
P94459
O32441
Q24444
Q24444
Q4444
Q9X8V6
075064
046979
051832
0962335
0963326
095714
066002
066003
P93403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Best Local Similarity 20.81
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
Q63829
Q63829;
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OF 3829
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048693 arabidopsis
088429 drosophila
088031 streptomyce
089031 streptomyce
099421 homo sapien
099450 mus musculu
09945037 mus musculu
028746 archaeoglob
0994517 thermotoga
099499 heliobacill
08846 sphingomona
020439 ceenorhabdi
091393 neurospora
001393 neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q63829 mus musculu
Q27512 caenorhabdi
Q9y6g5 homo sapien
Q08859 klebsiella
                                                                                                            May 15, 2000, 05:33:25; Search time 55.93 Seconds (without alignments) 277.684 Million cell updates/sec
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                                                                                                                                                                                                                    1 MSAVGAATPYLHHPGDSHSG.....ALVLKEMADLEKRCERRLQD 224
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             4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
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             GenCore version
Copyright (c) 1993 - 2000
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Listing first 45 summaries

    protein search, using sw model

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027512
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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sp_rodent:*
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Match Length DB
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seq length: 1000000
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418
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Total number of

searched:

Minimum DB Maximum DB

Database

Perfect score: Scoring table:

Sequence:

OM protein

Run on:

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88888 886.55 887.55 888.55 888.55 80.81

79.5

Score

Result

Last annotation update)

01-NOV-1999 (TrEMBLrel. 12,

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WILSON R., BAYNES C., BERKS M.,
WILSON R., BURGOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURGOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURGON J., CONNELL M., FYELLO A., FULTON L.,
GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAIRSTER M., LATREILLE P.,
JONES M., KERSHAM J., KIRSTEN J., LAIRSTER B., O'CALLAGHAN M.,
PARSONS J., LLOYD C., MUNTRARY A., MONTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONHHAMMER E., STADEN R., SULZINON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATENSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
T. D. O'C CONTIGUOUS NUCLEOCITÉE SEQUENCE from Chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 LDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SQRPLLDSVAQQQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 ---PNDFADDQEDL---KNIIRYGELFKACHAINSTDFIQKSEDLKDEEKVALERIVEQK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 GA-WLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRYSV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%; Score 93.5; DB 5; Length 676;
llarity 22.7%; Pred. No. 1.8;
Conservative 32; Mismatches 63; Indels 49
                                                                                                                                                                                                                                          Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Annexin; Calcium/phospholipid-binding; Repeat.
SEQUENCE 676 AA; 74969 MW; 00E36C79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 AA
                              676 AA
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                                                                Created)
                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00223; ANNEXIN; 1.
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                                                             01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00191; annexin; 4. PRINTS; PR00196; ANNEXIN.
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HSSP; P79134; 1AVC.
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                              PRELIMINARY;
                                                                                                                                            Caenorhabditis elegans.
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Best Local Similarity
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                                                                                                                NEX-2 PROTEIN.
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01-NOV-1999
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Q9Y6G5;
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52 LKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQ----QALRLPPTSLKPD 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 AWLPHVADFR------WRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVP 193
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                                                                                                                                                                                                                                         , MAO Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 89.5; DB 4; Length 20/2;
; Pred. No. 0.83;
44; Mismatches 81; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 413;
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"Identification and characterization of the genes encoding and type I fimbrial adhesins of Klebsiella pneumoniae.";
J. Bacteriol. 171:1262-1270(1989).
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                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=PITUITARY TUMOR;
FU G., HUANG Q., SONG H., PENG J., ZHANG Q., MAO M., DAI I ZHOU J., CHEN Z., CHEN J.;
"Human PID002 mRNA, complete cds.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF078857. AAA44489-11.
SEQUENCE 202 AA; 22966 MW; 51317189 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 11:1202-12/0(1393).

SEQUENCE FROM N.A.

NICHOLS N.W., CLEGG S.;

Submitted (AUG-1933) to the EMBL/GenBank/DDBJ databases.

EMBL: L23111, AAA25064.1; -.
                                                                                     Vertebrata;
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Last annotation update)
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26.8% Pred. No. 2.7;
iive 31; Mismatches 72;
                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 AA; 46940 MW; 8149AFC3 CRC32;
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Local Similarity 18.4%;
hes 38; Conservative 44
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Best Local Similarity 26.83
Matches 52, Conservative
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01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08),
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         [1]
SEQUENCE FROM N.A.
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Best Local Simi
Matches 56;
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0.1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 135.8 (ND PROTEIN.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                    :| |: | | | : | : | : : | : : | : : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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EMBL, ACO02396, AAACO0597.1; --
MENDEL, 27893, ARATh;3357;27893.

SEQUENCE 332 AA; 35831 MW; AOD178A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
       -AWL
                        PHV-ADFRWRVDVAISTSALARSLQP-----SVLMQLKLSDGSAYREEVPTAKFQELR
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Last annotation update)
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TFRDQLQELCIPQDLVGDLAS-VVFGSQRPLLDSVAQQQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.6%; Score 86.5; D 22.2%; Pred. No. 3; Live 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                  332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                 QPEGVARLVLEYAE 280
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Best Local Similarity
Matches 51; Conserv
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GRAZNI G., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G., AGBAYNI A., ARCAINA T.T., BAXTER E., BLAZEJ R.G., BUTENHOFF C., CHAMPE M., CHAVEZ C., CHEM M., DOYLE C.M., FARRAN D.E., FRISE E., GALLE R., GEORGE R.A., HARRIS N.L., HOSKINS R.A., EVANS.HOLM M., HOUSKINS R.A., EVANS.HOLM M., E., LI P., MOSHREFI M., PACLEB J.M., GELNIKER S.E., SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T., SUBMITTER G. MAR. 1999) to the EMBL/Genbank/DDBJ databases.

EMBL, AF132186; AAD34774.1; -.

SEQUENCE 1212 AA, 135812 MW; 518E0F63 CRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEQLGALLAGMHTILQQALRLPPTSLKPD-TFRDQLQELCIPQDLVGDLASVVFGSQRPL 137
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MEDLINE; 98325042.
LAI M.M., BURNETT P.E., WOLOSKER H., BLACKSHAW S., SNYDER S.H.;
"Cain, a chowel physiologic protein inhibitor of calcineurin.";
J. Biol. Chom. 273:18325-1833[1998).
EMBL; AF061947; AAC40176.1;
SEQUENCE 2182 AA; 242811 MW; F4CC8540 CRC32;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Last annotation update)
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7.6%; Score 85.5; D
Best Local Similarity 20.8%; Pred, No. 45;
Matches 49; Conservative 34; Mismatches
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27.2%; Pred. No. 17;
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KINNSHI H., HOPWOOD D.A.;
A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
MRL; AG031107; CAA19954.1; -.
Hypothetical protein.
SEQUENCE 218 Aa; 23670 MW; 19769615 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 VLMQLKLSDGSAYRFEVPTAKFQELRYSVALVLKEMADLEKRC------ERRLQD 224
                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
----LDSVAQQQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAY 188
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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27.1%; Pred. No. 3.6;
1ve 22; Mismatches 51; Indels
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PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEEGER K.J., HARRIS D.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
101-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 23.7 KD PROTEIN.
SCSA7.25C.
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Matches 48; Conservative 22;
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MEDLINE; 97000351.
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                                                                                                                                                                                                                                                                                                                                                                                                                           135 ISRIGSTINPFLDIPHDPNAAVYKSGFLARKIHADMDGKKTPRGKRGWKTFYAVLKGTVL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 SLOGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQAL---RLPPT-SLKPDTFRDQL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 QELCIPQDIVG----DLASVVF-----GSQ----RPLLDSVA---QQQGAWLPHV 152
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MEDLINE; 99246063.
NAGASE T., ISHIKAMA K., SUYAMA M., KIKUNO R., HIROSAWA M.,
NAGASE T., ISHIKAMA A., KOTANI H., NOWURA N., OHARA O.;
"Prediction of the coding sequences of unidentified human genes. XII
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:63-70(1999).
EMBL, AR023159; BAA76786.1; -.
SEQUENCE 418 AA, 47378 MW; 02662B38 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILNE; 99268151.
LEUNG C.L., SUN D., LIEM R.K.H.;
"The intermediate filament protein peripherin is the specific interaction partner of mouse BPAG1-n (dystonin) in neurons:"; Cell Biol. 144:35-446(1999).
EMBL; AF115383; AAD22959.1; -.
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8.6;
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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23.8%; Pred. No. 8.6;
tive 41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992 AA; 112950 MW;
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Best Local Similarity 22.4%
Matches 59; Conservative
                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 23.89
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYSTONIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9WU50:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaeoglobus.
                                                      Ouery Match
Best Local Simi
Matches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 14
                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                            028746
028746;
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                   386 ---GGWMLEGC----RISGGLKGDFLKKSVEPEASPSLDLNQACSVRDE--FFQFQGLRH 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 LPPLVEAATQSKEIRDAAASTARKL----IEALRGKHSGSGVEGLVQEYSLSSQEGVALM 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 LPP--EVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALL 86
                                                                                                                                                                                                                                                                            SIGNATURE ON STATE OF THE SECURATION OF THE STADISHMENT OF WEDELINE; 97157944.

JIMENEZ-ZURDO J.I., GARCIA-RODRIGUEZ F.M., TORO N.;

"The Rhizoblum meliloti puta gene: its role in the establishment of the symbtotic interaction with alfalfa.";

MOL. Microbiol. 23:85-93(1997).

EMBL; Y08500; CA869727.1;

PFAM: PF00171; aldedh; 1.

PFAM: PF01619; Pro_dh; 1.

SEQUENCE 1224 AA; 131190 MW; B2C95AEO CRC32;
 143 QQQGAWLPHVADFRWRVDVAISTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAEHR W., CHAMPAGNE M.S., IEE A.K., PITTLER S.J.;
"Complete CDNA sequences of mouse rod photoreceptor cGMP
phosphodissterase alpha- and beta-subunits, and identification of
beta'., a putative beta-subunit isozyme produced by alternative
splicing of the beta-subunit gene.";
EMBS. GAF1.278:107-114(1991).
EMBL: X87952; CAG61202.1; -
PROSITE; PS00126; PDEAE_I: 1.
                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 1224;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                 1224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 82; DB 28.1%; Pred. No. 44; tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  800 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TIEMBLREI. 01, Created)
01-NOV-1996 (TIEMBLREI. 01, Last sequence u
01-NOV-1999 (TIEMBLREI. 12, Last annotation
ROD PHOSPHODIESTERASE BETA SUBUNIT ISOZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 AGMHTLLQQALRLPPTSLKPDTFRDQLQE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C----LAERPVRIPDTATRDALIRDKIAD 127
                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                              :| :| : |: 437 TVTGRQLVEAKLLDMRTVEQLRL 459
                                               203 SVA---LVLKEMADLEKRCERRL
                                                                                                                                                        03,
03,
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 28.18
Matches 25; Conservative
                                                                                                                                PRELIMINARY;
                                                                                                                                                    01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                            Rhizobium meliloti.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                        PUTA GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                               P95629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q62037
Q62037;
                                                                                                      RESULT 11
P95629
ID P95629
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                                                                                                                                                                                                                                                                                                                                                           80 EQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLD 139
                                                                                                                                                                                                                                                32 EVAAMARLLGDLDRS-----TFRKLLKFVVSSLQGEDC-----RDGVQRLGVSANLPE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 98049343

KLENK H.-P. CLATTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
KICKHENBON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
KIRKNESS E.F., DOUGHEREY B.A., MCKENBY K., ADAMS M.D., LOFTUS S.,
KTRKNESS E.F., DOUGHEREY B.A., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU OVERBEEK R., GOCATNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARLLGDLDRS-----TFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMH 90
                                                                                                                                                                                                                                                                                     187 -----SYRFEVPTAKFQELRYSVALVLKEMADLEKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 SVAQ-----QQGAWLPHVADFRWRVDVAISTSALARSLQ-----PSVLMQLKLSDGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 HVAQTKKMINVQDVAECPHFSSFADELTDYVTKNILSTPIMNGKDVVAVIMAVNKLDGPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                      Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 145;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                   DB 11;
                                                                                                                                                                                                       68;
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PFAM; PF00233; PDEASE; 1.
PRINTS; PR00387; PDIESTERASE1.
SEQUENCE 800 AA; 92076 MW; 3204E9D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E5041F32 CRC32;
                                                                                                                                          Similarity 19.4%; Score 81.5; D
Similarity 19.4%; Pred. No. 28;
9; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
7.2%; Score 81; DB 1
Best Local Similarity 30.7%; Pred. No. 3.2;
Matches 35; Conservative 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l protein.
145 AA; 16339 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeoglobus fulgidus.
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Job time:
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE: 99287316.

MELSON K.E., CLAATON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
NRLSON K.E., CLAATON E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., FRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HIDDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.;
"Evidence for lateral gene transfer between Archaea and bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 LAAVAGRIQVFIYIPGIKSSERIHSLGSELQDKQQEIERKILELERQ-----LKTETDPL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
NELSON K.E., CLAYTON R.A., GILL S.R., DELSON W.C., KETCHUM K.A.,
HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHWANN R.D., WHITE O., SALZBERG S.L.
SWITH H.O., VENTER J.C., FRASER C.M.,
SUDMITTED (JUN1999) to the EMBL/Genbank/DDBJ databases.
EMBL, AE001744, AAD35819.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSAVGAATP-YLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSL 59
27
MERILLVLDDTGRGEIAFQKLKKLAEDGLRGEVYILYIREMEVPPFVPEEK---ELAAYH
                             TLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQ 144
                                               Query Match

7.1%; Score 80.5; DB 2; Length 161;
Best Local Similarity 27.7%; Pred. No. 4.1;
Matches 26; Conservative 20; Mismatches 35; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHELICAL 18.1 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reliobacillus mobilis.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Heliobacterium group; Heliobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 AA; 18092 MW; B3E9F115 CRC32;
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                                                                                                                                            161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last seq 01-MAY-1999 (TrEMBLrel. 10, Last ann EXOPOLYPHOSPHATASE PPX (FRAGMENT).
                                                                                                                                                                                                                                                      Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 99061957.
XIONG J., INOUE K., BAUER C.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                            PRELIMINARY;
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SEQUENCE 16
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                                                                                                                                            Q9WZJ7
Q9WZJ7;
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Q92GG9
                                                                                                                RESULT 14
                                                                                                                                  09WZJ7
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137 -----RIPVVVDIGGGSAEVVF-------HHKDRWWROSFPLGAVR 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 LTESPLGRVDIASVWAPAVEKVSSLQRMGRPILIGVGGTITTVAAIALOLRDYAPDKVHG 230
                                                                                                                                                                                                                                                                                                                                                             56 VS----SLOGED-CRDGVQRLGVSANLPEEQLGALLAGM---HTLLQQALRLPPTSLKPD 107
                                                                                                                                                                                                                                                    ----TERKLLKFV 55
                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                  27 GKQTPLWHHLDTIRLGREVIRSGILHPD--AVERIMAALGHGVESMQKYGISVQQVAAFA
                                                                                                                                                                                                              196
                                                                                                                                                                                                                                                                                                                                                                                                              108 TFRDQLQELCIPQDLVGDLASVVFGSQRPLLDSVAQQQGAWLPHVADFRW---
                                                                                                                                                                   Query Match
Pest Local Similarity 22.0%; Pred. No. 11;
Matches 59; Conservative 32; Mismatches 81; Indels
                                                                                                                                                                                                                                                    5 GAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRS-----
                                                                                         NON_TER 1 1 SEQUENCE 311 AA; 33883 MW; B91E34DE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 FEVPTAKFQELRYSVALVLKEMADLEKR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: May 15, 2000, 05:33:29
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Mon May 15 14:56:42 2000

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RESULT
W37723
                                                                                                  May 14, 2000, 23:18:10 ; Search time 38.86 Seconds (without alignments) 136.533 Million cell updates/sec
                                                                                                                                                                     US-09-223-796-2
1112
1 MSALGAAAPYLHHPADSHSG......ALVLKEMAELEKKCERKLQD 224
                                                                                                                                                                                                                                                                                                                                   188963
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              188963 seqs, 23686106 residues
                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_36:*
                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                               Run on:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	at Hypertensi	. pneumoniae	S. pneumoniae pept	Amino acid sequenc	Human secreted pro	P. falciparum live	Pseudomonas pseudo	Moraxella catarrha		Polypeptide of hum	Human WIS mature p	q papooue eucoded p	Human MIS protein.	Bacillus subtilis	Mature Pseudomonas	Staphylococcus aur	Mature Pseudomonas	sati		Miniature swine re	н	Zuenl	Human Zneul partia		Human neuro-growth	mitogen-				•	Human mitogen acti	Human 160kD mediat	Truncated restin p	Mature Pseudomonas
SUMMARIES																																			_
SUM	ព		W29380	W38592	W71684	_	2	5392	W46270	R75189	P90476	R76502	P70196	R76501	R34712	R88023	W97720	R88021	W48309	Y13349	W32097	W39272	W88390	W88391	W88382	W88381	W06320	W97670	W06321	W97671	32	57	53	W41586	02
	DB			_					н	-	Н	-	-	-	н	-	Н	-		Н	Н	Н	-4	-									~		
	ength	;	359	359	195	196	1786	289	758	1196	427	536	559	260	3588	289	1048	289	875	9	1145	1194	169	181	254	273	363	363	393	393	399	399	1427	687	289
d	atch	100.0	ω,				7.6	7.4			7.4	7.4			7.3	7.2	7.2	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1						7.1	•	•
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			1 6	ım	4	· LC	o ve	^	. α	o	0.0	,	12	13	14	15	16	17	œ.	6.	20	2.5	22	23	24	25	26	27	200	60	30	3.1	32	33	34

Mature Pseudomonas eryA region polype	Mature Pseudomonas	Polymerase ennanci Notch hN3k full le	Human BAZ1-beta pr	Huntingtin interac	Huntingtin interac	Angiotensin, New C	Mycobacterium tube	Mycobacterium tube	
R88024 R44431	R88022	W72844 R28963	W81172	W18029	W18030	P50636	W32425	W32357	ALIGNMENTS
н н	1		ı –ı	Н	Н	Н	Н	Н	
289	289	403	1527	388	914	477	344	344	
7.0	6.9	0 0 0	9.0	8.9	6.8	9.9	6.7	6.7	
77.5	76.5	76.5	76.5	97	16	75.5	7.5	75	
35	37	38	40	41	42	4.3	44	45	

RESUI	1 T
ID	W37723 standard; Protein; 224 AA.
2 E	-JUN-1998 (first entry
DE	
¥ 3	extracellular calcium concentration; antibody; hypertension;
ΚW	hyperthyroidism; osteoporosis; heart fallure; diabetes; stroke;
X C	cancer; inflammatory disease; astuma.
2 5	Rattus fattus.
4 E	
FT	/note= "EF-hand like motif"
PN	W09749807-A2.
<u> </u>	31-067-1997
PF D	23-40N-129V; CAU45.9-
PA	(GOSSA) GOSSARD F.
PA	(HAME/) HAMET P.
PA	(LEWANZ) LEWANZOUK R.
P.P.	(IKEM) Interpolation of Tremplay J.
DR.	07.
DR	
PT	
PT	e.g. nypertension,
F C	Osteoporosis, near latture, cancer, crosses or common of the property of the concept of the conc
بر در	Ciaim o, rayes v. 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.
ខ្លួ	requiated gene (HCaRG), which was isolated from the rat parathyroid.
ខ្ល	Its expression is regulated by extracellular calcium concentration.
ပ္ပ	An antibody against the protein, can be used to detect of mountain
ខ្លួ	(e.g. ennance or innibit) abmormmar carciam recass
ខ្លួ	byperthyroidism, osteoporosis, heart failure, diabetes, stroke, cancer,
88	inflammatory disease, and asthma.
ÖS	Sequence 224 AA;
õ	Query Match 100.0%; Score 1112; DB 1; Length 224;
ăï	Similarity 100.0%; 4; Conservative 0;
ò	1 MSALGAAAPYLHHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALH 60
;	
8	
QY	61 GKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALKLPPASLKPDAFQEELQELGIPQ 120
g	61 GKDCREAVEQLGASANLSEERLAVLLAGTHTILLQQALRLPPASIKPDAFQEELQELGIPQ 120
QY	121 DLIGDLASLAFGSORPLLDSVAQQGGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLWQL 180
Q	121 DLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVALSTSAQSRSLQPSVLMQL 180
ò	181 KLTDGSAHRFEVPLAKFOELRYSVALVLKEMAELEKKCERKLOD 224
ž	

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Wri: 92-000/34/01.

PT N-PSDB: T89027

PT Procuding peptide releasing factor, RF-1 from Streptococcus

Procudiniae - useful for diagnosis and treatment of, e.g. otitis

Procudioniae - useful for diagnosis and treatment of, e.g. otitis

Claim 12; Page 9; 41pp: English.

Completed polypetide relation and pacterial traget. RF-1 can be used to centrate of thishit cell division through a novel regulatory circuit.

Claim 12; Page 9; 41pp: English.

Claim 12; Page 9; Protect the animal from disease.

Claim 12; Page 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. preumoniae peptide reléasing factor RF-1.
RF-1; peptide releasing factor; Streptococcus pneumoniae; diagnosis; otitis media; conjunctivitis; meningitis; pneumonia; endocarditis;
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                                                                                    W29380 standard; Protein; 359 AA.
W29380;
                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9743304-A1.
20-NOV-1997.
14-MAY-1997; U08272.
14-MAY-1996; US-017670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98-008794/01.
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WPI; 98-008
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RESULT
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                                      11;
                                                                                                                             EYEEKLKILLLPKDPNDDKNIILEIRGAAGGDEAALFAGDLLTMYQKYAEAQGWRFEVWE 152
                                                    48 FRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPD 107
                                      Gaps
                                                                        53 YKQVLQNIV-----DAEEMIKESGGDADLEE------LAKQELK--DAKAEKE 92
                                                                                                     108 AFQEELQELGIPQD-----LI-----GDLASLAFGSQRPLLDSVAQQQG-----
                                                                                                                                                     SSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFE-VPIAKFQ---ELRY
                                                                                                                                                                     55;
      8.9%; Score 99.5; DB 1; Length 359;
24.6%; Pred. No. 0.054;
1ve 37; Mismatches 58; Indels 5;
                 0.054;
-hes 58; Indels
                                                                                                                                                                                                        203 SVALVLKEMAELEKKCERK 221
                                                                                                                                                                                                                       : ||: |: |: |
ATVLVMPEVEEVEYDIDPK 221
                                 Conservative
Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                               93
                                                                                                                                                       147
                                                                                                                                                                                                                               203
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8 à g ö g ò g W38592 standard; Protein; 359 AA.

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Claim 12; Pages 359-360; 483pp; English.

This sequence represents a Streptococcus pneumoniae protein that, based on homology with a Bacillus subtilis protein, is a peptide chain release factor 1, and is encoded by a DNA sequence of the invention.

The DNA sequences were islandated from Streptococcus pneumoniae strain (100993 (NCIMA 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to identify compounds which interact inth and invention. They can alsb be used to induce an immunological response of the encoding nucleic acids in a vector adequate to produce antibody and and or I call immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloaritors in particular the proteins of extracellular matrix proteins on in-dwelling devices or in mammalian con progression of pathogenesis in infections initiated other than by the infections in implantation of in-dwelling devices or other than by the inferiors.
                                       S. pheumoniae peptide chain release factor 1. Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; r cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 FRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPD 107
                                                                                                                                                                                                                                                                                                                                                                                                            useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 YKQVLQNIV------DAEEMIKESGGADLEE------LAKQELK--DAKAEKE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                 Novel Streptococcus pneumoniae proteins and related DNA - u
diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,0.054;
-hag 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%; Score 99.5; DB 1;
24.6%; Pred. No. 0.054;
                                                                                                                                                                                                                    20-NOV-1997.
14-MAY-1997, U07950.
14-MAY-1996; US-017670.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT. Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.68;
                          (first entry)
                                                                                                                                                                      Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.00
                                                                                                                                                                                                                                                                                                                                                                                               Novel Streptococcus
                                                                                                                                                                                                                                                                                                                                                          WPI; 98-008793/01.
N-PSDB; T98642.
                                                                                                                                                    pathogenesis.
                                                                                                                                                                                       W09743303-A1.
                                                                                                                                                                                                                                                                                                                                      Stodola RK;
                                                                                                                                                                                                             0-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                           infections
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147 SSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLIDGSAHRFE-VPIAKFQ-----ELRY 202 93 EYEEKLKILLLPKDPNDDKNIILEIRGAAGGDEAALFAGDLLTMYQKYAEAGGWRFEVME 152 W11684 standard; Protein; 195 AA. W71684; 04-DEC-1998 (first entry) Amino acid sequence of the human tumourigenesis associated protein. Human; tumourigenesis associated protein; HTAP; transplantation; 153 ASMNGVGGFK---EVVAMVSGQ-----SVXSKLKYESG-AHRVQRVPVTESQGRVHTST 108 AFQEELQELGIPQD-----LI-----GDLASLAFGSQRPLLDSVAQQGG-SVALVLKEMAELEKKCERK 221 ATVLVMPEVEEVEYDIDPK 221 203 203

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New tunorigenesis-associated protein and related nucleic acid,
vectors, transformed cells - antibodies, agonists and antagonists,
for diagnosis, treatment and prevention of abnormal cellular
differentiation, particularly cancers and inflammation

To diagnosis, treatment and prevention of abnormal cellular
differentiation, particularly cancers and inflammation.

This is the amino acid sequence of the human tumourigenesis
associated protein (WTMP), used in the method of the invention. HTMP,
as involved with cell proliferation and inflammation. It can be used
to stimulate cell proliferation (e.g. of cells intended for
to stimulate cell proliferation (e.g. of cells intended for
transplantation in treatment of tumours or infections, or to treat
genetic defects). Antagonists of HTMP are used to treat or prevent
a wide range of cancers (adenocarcinoma, melanoma, sarcoma, lymphoma,
leukaemia etc.), also inflammation where associated with infection or
amunological disease (e.g. asthma, cystic fibrosis, rheumatoid
arthitis). HTMP is also used to raise antibodies are used as for
diagnosis or monitoring of HTMP-related diseases (in usual
immunoassays), in competitive drug screens and to isolate HTMP-related
diseases; to identify related sequences; for genomic mapping and for
standard amplification or hybridisation tests to diagnose HTMP-related
diseases; to identify related sequences; for genomic mapping and for
screening for specific inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ώ
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Human secreted protein; treatment; prevention; protein therapy; AIDS; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder. leukemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia; cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis; arthritis; malignancy; digestive; endocrine; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 RLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ATYILEAGKHRADKSTL---STYLEDCKFDRERIELFCTE------YQNNKNSLEI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 VAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKL--TDGSAH---RFEVPIA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EQLGASANLSEE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 OMLADPRSFDSNAFTLLLRAAFQSLLDAQADEAVLDHPDLKHIDPVVLKHCHAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.8%; Score 86.5; DB 1; Length 195;
st; cancer; inflammation; immunological dis
primer; PCR; amplification; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 QLLKD---LDRSTFRKLLKLVVGALHGKDCREAV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.8%; Score 86.5; D
Best Local Similarity 22.1%; Pred. No. 0.44
Matches 46; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 KFQELRYSVALVLKEMAELEKKCERKLQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y07867 standard; Protein; 196 AA
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                                                                                                                                                                                           (INCY-) INCYTE PHARM INC
                                                                                                                                                                    US-822260
                                                                                                                                                                                                                    Goli SK, Hillman JL;
WPI; 98-521224/44.
  Antagonist;
                                                                                                                                           20-MAR-1998; U06066
20-MAR-1997; US-822:
                         antibody; probe;
                                                                                                                                                                                                                                                               N-PSDB; V58281
                                                                                             WO9841635-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                           Homo sapiens
                                                                                                                    24-SEP-1998
                                                nhibition
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preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, prostate disease, skeletal or cardiac muscle disorders, pulmonary disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplant rejection, disorders involving osteoclasts such as osteoprosis, arthritis or malignancies, digestive/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in Y07852-Y07993 and the encoding nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptides they encode Claim 1b; Page 285-286; 368pp; English.
This invention describes novel isolated human genes and the secrete proteins they encode. The products of the invention are useful for
                                                                                                                                                                                                                                                                            Carter KC, Duan DR, Endress GA, Feng P, Ferrie AM, Florence KA, Greene JM, Janat F, Lafleur DW, Ni J, Rosen CA, Ruben SM, Shi Y, Young P, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 AA;
                                                                                                                                                                                                                                                         HUMAN GENOME SCI INC.
                                                                                                                 US-060837.
US-060839.
US-060843.
US-060862.
US-060866.
US-060866.
                                                                                                                                                                                                                                                                                                                                     99-264022/22.
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; X37466
                                                                                                                                                       02-OCT-1997;
                                                                                                                                                                                                                      02-OCT-1997;
                                                                                                                                                                                                                                    02-OCT-1997;
                                                                                                                                                                                               02-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                           (HUMA-)
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Gaps Indels 47; Length 196; 82; Query Match 7.8%; Score 86.5; DB 1; Best Local Similarity 22.1%; Pred. No. 0.45; Matches 46; Conservative 33; Mismatches 82; 46;

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67 ATYILEAGKHRADKSTL---STYLEDCKFDRERIELFCTE-----YQNNKNSLEI 113 38 QLLKD---LDRSTFRKLLKLVVGALHGKDCREAV------EQLGASANLSEE 80 67 12 OMLADPRSFDSNAFILLLRAAFQSLLDAQADEAVLDHPDLKHIDPVVLKHCHAAA----81 RLAVLLAGTHTLLOQALRLPPASLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDS ð g δ g

141 VAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKL--TDGSAH---RFEVPIA 195 ò g

196 KFQELRYSVALVLKEMAELEKKCERKLQ 223 οχ g

W24790 standard; Protein; 1786 AA. W24790; RESULT.
W24790
ID W247
AC W247
AC W247
DT 08-0
DE P. E
KW Plas
KW Prop

9

08-0cT-1997 (first entry)
P. falciparum liver stage antigen-3.
Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophylaxis; Thai strain, gene organisation; exon; intron, hydrophobic; glycosyl-phosphatidylinositol membrane anchoring sequence, antibody;

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                                                                                                                                                                                                                                                                            Claim 1: Fig 2A-T; 69pp; French.

This sequence corresponds to a plasmodium falciparum strain K1

This sequence corresponds to a plasmodium falciparum strain K1

This sequence corresponds to a plasmodium falciparum strain T996

This sequence was isolated by screening a P. falciparum strain T996

Ibrary with serum from a missionary treated by prophylaxis (for strain T6/96 see F89101286). Of 20 clones isolated, clone 795 was used to creen a library generated from Thai strain K1. One clone contained a Screen a library generated from Thai strain K1. One clone contained a Screen a library generated from Thai strain K1.

Screen a library generated from Thai strain K1. One clone contained a Screen a library generated from Thai strain K1.

Screen a library generated from Thoseks of tecrapeptide repeats

(a 95 kb insert including the genomic sequence T78867. The gene comprises (a precially the amino acid sequence VEES, VEEN, VEEN, VAPY, etc.)

and a 3' hydrophobic region corresponding to a glycosyl-phosphatidyl-
colypeptides of at least 10 amino acids derived from the LSA-3 protein

with the exception of the peptides W34791-4. The LSA-3 protein

with the exception of the peptides W34791-4. The LSA-3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LMKDAVEINDITSK---LIETQELNEVEADLIKDMEKLKELEKALSEDSKEIID 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || : |: | :||: || 1341 ILEDYKELKTIETDILBEKKEIEKDHFEKFEEEAEEIKDLEADILKEVSSLEVEEERKLE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 AGTHTLLQQALRLPPASLKPDAFQEELQELG-IPQDLIGDLASL------AFG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LIDGSAHRFEVP---IAKF----QELRYSVALVLKEMAELEKKCERKLQ 223
                                                                                                                                                                                               Daubersies P, Druilhe P; WPI; 97-065464/06. WPI; 97-065464/06. WPI; 97-065464/06. Presponding try 178868. Plasmodium falciparum poly:peptide(s) and related nucleic acids -derived from the liver stage antigen-3, useful for malaria vaccine prodn. and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 SQRPLLDSVAQQQ---GSSLPHVSYFRWRVDVALSTSAQSRSLQPSVLMQLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 SQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W53924;
20-AUG-1998 (first entry)
Pseudomonas pseudoalcaligenes lipase variant.
Lipase variant; improved wash performance; removal; lipid stain;
reduced calcium dependence; one-cycle wash efficiency; detergent;
cleaning composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%; Score 84.5; DB 1; Length 1786;
21.6%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Mismatches 79; Indels
                                                                                   5
                                                                                   /note= "repeat region
1537. .1576
                                                      /note= "repeat region
                                                                                                             /note= "repeat region
                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W53924 standard; peptide; 289 AA.
 immunotherapy; malaria
                                                                    279. .818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 21.69
Matches 52; Conservative
                                                                                                                                                    12-JUN-1996; F00894.
13-JUN-1995; FR-007007.
(INSP ) INST PASTEUR.
             falciparum
             Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1401 E 1401
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performance in detergent formulations, maying improved wash performance in detergent formulations (claim 52, Page -: 104pp; English.

The present sequence represents a variant of a wild-type Pseudomonas pseudoalcaligenes lipase. The variant lipase has have better wash performance than the original lipase. It has improved removal of lipid stains, reduced calcium dependence, better compatibility with detergents or their components, increased hydrophobicity, altered substrate specificity and better one-cycle wash efficiency. The variant lipase is used in detergent and cleaning compositions.

In a sequence does not appear in the specification; it was created using information provided. 73 ASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQDLIGDLASL--- 130 74 AISGKGKVNLVGHSHGGPTVRYVAAVRPDLVASV----TSVGAPHKGSDTADFIRQI- 127 127 PPGSAGEAIVAGIVNGLGALINFLSGSSSTS-------PQNALGALESLKSE 171 130 ---AFGSQRP--LLDSVAQQGGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLM--QLKL 182 39; Gaps 15 ADSHSGRVSFLG-SQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALH-GKDCREAVEQLG 72 amino acid /note= "Leu optionally replaced with Ile of DB 1; Length 289 /label= 12681 /note= "Leu optionally replaced with Ile" /label- D2728 /note- "Asp optionally replaced with Ser" 275 /note= "Val optionally replaced with Pro" /label= \$224T /note= "Ser optionally replaced with Thr" Ala" /label= #242R /note= "His optionally replaced with Arg" Met. /note= "Asp optionally replaced with Asn" /label= T275S /note= "Thr optionally replaced with Ser" 286 Indels Variants of lipse from Pseudomonas containing specific substitutions - deletions or additions, having improved /label= D229G /note= "Asp optionally replaced with /label= P231A /note= "Pro optionally replaced with /label- K245M /note- "Lys optionally replaced with 75; Query Match 7.4%; Score 82.5; D Best Local Similarity 26.3%; Pred. No. 1.9; Matches 49; Conservative 23; Mismatches Location/Qualifiers Pseudomonas pseudoalcaligenes label- v216P /label- D250N /label- L286x 29-AUG-1996; US-029190. 27-AUG-1996; DK-000902. (NOVO) NOVO-NORDISK AS. OKKels JS, Svendsen A; WPI; 98-230259/20. Misc_difference 245 26-AUG-1997; DK0345 Misc_difference 216 Misc_difference 229 Misc_difference 242 Misc_difference 250 Misc_difference 268 Misc_difference 224 Misc_difference 272 Misc_difference 23 Misc_difference Misc_difference Sequence

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142 -----AQQQGSSLPHVSYFRWRVDVALSTSAQSRSLQPSVLMQLKLTDGSAHR 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 VAAIAVLTKDAGKLTMGQ--PLVILAPHAE---EALVKQPPDRWLSNARMTHYQAMLLDT 587
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------GASANLSEERL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osteoinductive retrovirus RFB-14 pol gene product.

RFB retrovirus; gag; pol; env; osteogenesis; osteoinductive protein; bone development; osteoporosis; gene therapy; polymerase; reverse transcriptase.

REtrovirus RFB-14.

DE4411713-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 VTAVAQLLKDLDRSTFRKLLKLVVGALHGKDCREAVEQLGASANLSEERL----AVLLAG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIB-14 retrovitus genome - and prodn. of osteo-inductive proteins claim 14; Fig 1; 46pp; German.
The full-length provital genomic sequence of retrovitus RFB-14 has been determined. The virus codes for an osteoinductive protein. although the precise location of the coding region has not yet been identified. The virus may be useful in gene therapy of bone growth disorders such as osteoporosis. The present sequence is that of the viral pol gene product.
This protein comprises the CopB outer membrane protein of Moraxella catarrhalis strain 012E, encoded by an isolated copB gene (see V65360). CopB represents an important antigenic determinant of M. catarrhalis, and a specific epitope (see W46250-51) has been identified in the non-conserved region 1 of strains 012E and 035E that is bound by monoclonal antibody 10F3. Claimed peptides (see W46274-81) of this region can be used in the diagnosis, treatment and prophylaxis (as vaccines) of M. catarrhalis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 THTLLQQALRLPPASLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pedersen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1196;
                                                                                                                                                                                                                                                                                                                                             Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 AVLLAG---THTLLQQALR-----LPPASLKPDAFQEELQELGIPQDLIGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1994; 411718. 05-APR-1994; DE-411718. 05-APR-1994; DE-41178. 05-APR-1994; DE-41178. 05-APR-1994; DE-41178. 05-APR-1994; DE-41178. 05-APR-1994; 
                                                                                                                                                                                                                                                                                                                                          7.4%; Score 82.5; DB 1; 22.5%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------REAVEOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 DSHSGRVSFLGSQPSPE----VTAVAQLLKDLDRS--
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24.2%; Pred. No. 13;
Ive 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 -----WGALHGKDC----
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Best Local Similarity 24.2*
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt J, Strauss P; WPI; 95-352078/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1196 AA;
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             Query Match
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        888888888888
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  172 GAAAFNAKYPQGIPTSACGEGAYKVNGVSYYSWS-----GTSPLINVLDPSDLLLGATSL 226
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    .270
    /note= "approximate location of conserved region"
    275. .302

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "approximate location of conserved region"
                                                                                                                                                                                                                                                                                                                                       Moraxella catarrhalis strain 012E CopB outer membrane protein. CopB gene; outer membrane protein; epitope; infection; diagnosis; therapy; vaccine.

Moraxella catarrhalis strain 012E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-conserved
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region 9"
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485..486.
/note= "approximate location of region 6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "approximate location of
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(TEXA ) UNIV TEXAS SYSTEM.
Aebi C, Cope LD, Hansen EJ;
WPI; 98-159542/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          645. .680
/note= app
683. .695
/note= app
                                                                                                                                                                                                                                                                                                             17-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .480
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12-AUG-1997; U14221
                                                       183 TDGSAH 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-1987
                                                                                                                                                                                                                                                                                  Query Match
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641 WYSDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAEL-IALTQALKMAEGK--R 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 LOALLFGDDHRCFTRWTPALLLLPRSEPAPLPAHGOLDTVPFPPRPSAELEESPPSADP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---THTLLQQALRLPPA-----SLKPDAFQEELQELGIPQDLI--GDLASL--AFGSQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleaved dimers of Mullerian inhibiting substance like polypeptide(s) are useful in treating cancers and for contraception.

Claim 7(b); page 38; 64pp; English.

Monomer of an N-terminal dimer of Mullerian inhibiting substance
They are made by cleaving between Arg-Ser in the sequence
agrsag. The dimers are used to treat cancer,

Sep. female genital tract cancer, and for contraception. See also:
N90395 and P90475-8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human MIS mature protein."
Multerlan inhibiting substance; MIS; ovary cancer; therapy.
Homo sapiens.
USS427780-A.
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                                                                                                                                                                                                                                                                      Polypeptide of human Mulierian inhibiting substance. Mullerian inhibiting substance; human; cancer; contraception; N-terminal dimers.
                                                                                       698 LNV----YTDSRYAFATAHIHGEIYRRGLLTSEGREIKNKSE 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
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                                                                                                                                                                                                      standard; peptide; 427
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                                                                                                                                                                                                                                                   (first entry)
                                        190 FEVPIAKFQELRYSVA----
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Best Local Similarity 23.5%
Matches 54; Conservative
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28-OCT-1986; US-923879.
25-APR-1991; US-693764.
05-OCT-1992; US-957061.
(BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1989.
25-JAN-1989; U00239.
25-JAN-1988; US-281301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOJ) Biogen. Inc.
Cate R L; Pepinsky R B.
WPI; 89-233849/32.
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human).
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30-OCT-1985; 792880.
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LOALLFGDDHRCFTRMTPALLLLPRSEPAPLPAHGQLDTVPFPPPRPSAELEESPPSADP 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---THTLLQQALRLPPA-----SLKPDAFQEELQELGIPQDLI--GDLASL: -AFGSQ 134
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                                                                               for
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Cuber V.

Cate M.

WPI, 95-23996/31.

Compsn. comprising human Mullerian Inhibiting substance - useful ror treating cancer. esp. ovarian cancer.

Claim 1; Columns 7-8; 41pp; English.

The insert of bovine MIS cDNA clone p521 was used to isolate the human MIS gene from a cosmid library. The sequence of the encoded mature human MIS protein is given in R76502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-APR-1991 (first entry)
Sequence encoded by human mullerian inhibiting substance (MIS) gene
in cosmid clone chmis33.
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Bovine MIS protein from bovine testes was purified and the AA sequence of several fragments detd. Based on these protein sequences, several antisense oligonucleotide DNA probes were synthesised. The probes were then used to screen a bovine (DNA 11brary. The insert of one bovine MJS cDNA clone (pS21) was used to isolate the human MIS gene from a human cosmid library and partial cDNA clone from a human cDNA library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-tumour; cancer therapy; ovarian cancer; contraceptive
                                                                                                                                                                                                                                                                                                                                              DB 1; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence encoding Mullerian inhibiting substance-like polypeptide - for use in treatment of cancer, esp. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 559;
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Best Local Similarity 23.5%; Pred. No. 5.1;
Matches 54; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                           7.4%; Score 82; 23.5%; Pred. No.
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(GEHO-) GEN HOSPITAL CORP.
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30-OCT-1985; US-792880.
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nes 54; Conserv
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148 SLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQ----- 199
Bacillus subtilis
Mulienzyme complex
                    Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---THTLLQQALRLPPA----SLKPDAFQEELQELGIPQDLI--GDLASL--AFGSQ 134
                   229 LQALLFGDDHRCFTRMTPALLLLPRSEPAPLPAHGQLDTVPFPPPRPSAELEESPPSADP 288
                                      134
                                                        289 FLETLITRLVRALRVPPARASAPRLALDPDAL-----AGFPOGLVNLSDPAALERLLDGE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 PSPEVTAVAQLL---KDLDRSTFRKLLKLVV----GALHGKDCREAVEQLGASANLSEER 81
                                                                                                                                                                                                                                                                                                                                                               Compsn. comprising human Mullerian Inhibiting substance - useful for
                                                                                                                                                                                                                                                                                                                                                                      treating cancer, esp. ovarian cancer.
Disclosure; Fig.6a-6k; 41pp; English.
The insert of bovine MIS cDNA clone p521 was used to isolate the human MIS gene from a cosmid library. The DNA can be operatively linked to expression control sequences and used in mammalian or sequence 560 AA;
                                      ---THTLLQQALRLPPA-----SLKPDAFQEELQELGIPQDLI--GDLASL--AFGSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 RPLL-------DSVAQQGSSLPHVSYFRWRVDVAI-STSAQSRSL 172
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                                                                                        135 RPLL------DSVAQQQGSSLPHVSYFRWRVDVAI-STSAQSRSL 172
                                                                                                                                                                                     ovary cancer; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.4%; Score 82; DB
23.5%; Pred. No. 5.1;
ive 17; Mismatches
                                                                                                                                                                                                                  25. .536
/label= Mat_protein
/note= "Claim 1, column 26"
                                                                                                                                                                           Human MIS protein.
Mullerian inhibiting substance; MIS;
                                                                                                                                                                                                       Location/Qualifiers
25. .536
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                                                                                                                                               R76501 standard; Protein; 560
                                                                                                                                                                                                                                                     27-JUN-1995.
30-CCT-1985, 792880.
30-CCT-1985, US-792880.
28-CCT-1986; US-923879.
25-APR-1991; US-93764.
05-CCT-1992; US-957061.
(BIOJ) BIOGEN INC.
(GEHO) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R34712;
17-AUG-1993 (first entry)
                                                                                                                                                                  19-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                Cate RL, Donahoe PK;
WPI; 95-239996/31.
N-PSDB; 092785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAVLLAG-----
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                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                         R76501;
                                                                                                                                                                                                                  protein
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Matches
                                                                                                                             RESULT 13
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ID R3
AC R3
DT 17
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pharmaceutical prods.

The Bacillus subtilis chromosomal DNA region comprises the srfA claim 15, Page 27-34; 70pp; English.

The Bacillus subtilis chromosomal DNA region comprises the srfA operon which encodes the multienzyme complex surfactin synthetase coding for proteins, a zone upstream of the first ORF contg. the stafA operon promoter and a presumed terminator positioned downstream of the stop codon of the fourth ORF. ORF1 encodes a protein cart homology of ca. 1000 bases, more marked in the second half of internal homology of ca. 1000 bases, more marked in the second half of these regions. At the C terminal end of module 3 there is a region through ORF1 codes for a protein of unknown function, regions of the protein are found to be highly homlogous to synthetases coded by TycA and OrSA (tyrocidin and gramicidin synthetase subunits 1) and with complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2279 IKELDGELPVLTLPTDYSRPAVQTFEGDRIAF -- SLEAAKADALRRLAKETDSTLYMVLL 2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2337 ASYSAFLSKICGODDIIVGSPVAGRSQADVSRVIGMFVN-------TL---AL 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 RLPPASLKPDA-FQEELQELGIP-----QDLIGDLASLAFGSQRPLLDSVAQQQGS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KLVVGA-LHGKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQAL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSALGAAAPYLHHPAD-----SHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLL 52
ubtilis srfA operon ORF1 prod.
complex; surfactin synthetase; MCSS; ORF; surfactant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multi-enzyme complex surfactin synthetase DNA - is isolated Bacillus subtilis, and used for prodn. of surfactin for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perego M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                       /note= "repeat sequence"
1184. .1190
/note= "repeat sequence"
                                                                                                                                                                                                                                                                          /note= "mppeat sequence"
606. .616
/note= "repeat sequence"
                                                                                                                                                                                                                                                                                                                                                                  "repeat sequence" 2709
                                                                                                                                                                                                 2223. .2229
/note= "repeat sequence"
3255. .3261
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⁄note= "repeat sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                 sednence,
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note= "repeat sequence"
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                                                                           Location/Qualifiers
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858. .880
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2930, 2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1919
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Cosmina P,
                                                                                                                                                                                                                                                                                                                                                                                  note=
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02-SEP-1992; IT-MI2044.
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Best Local Similarity
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Carrera P, Cosmina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3588 AA;
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WPI; 93-145447/18.
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R88019-R88025 are protein variants of Pseudomonas pseudoalcaligenes r88019-R88025 are protein variants of Pseudomonas pseudoalcaligenes in page of the sequences are based upon the wild-type P. pseudoalcaligenes sequence disclosed in w09402617-4 (Gist-Erocades). The lipses variants can pe modified in a such amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules. The lipase variants show improved in-the-wash lipolytic activity and may sequence 289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
 02-AUG-1996 (first entry)
Mature Pseudomonas pseudoalcaligenes lipase L210R variant.
Mutant; lipase; enzymatic detergent; substitution; variant; improved;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 ASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQDLIGDLASL--- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 PPYSAGEARVAGIVNGLGALINFLSGSSSTS------PQNALGALESLNSE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AFGSQRP--LLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLTD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 ADSHSGRVSFLG-SQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALH-GKDCREAVEQLG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note- "possible site for Val to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "possible site for Ile to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note- "possible site for Gly to Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "possible site for Ile to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "possible site for Ser to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "possible site for Thr to Phe substitution"
                                                                                                                                                                                                                                                                                                       /label= substitution
/note= "Leu to Arg, in wild-type sequence a Leu
residue is present at position 210 of mature
P. pseudoalcaligenes lipase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suerbaum HMU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 80.5; Di
25.9%; Pred. No. 2.9;
tive 24; Mismatches
                                                                   2474 GGLTFVLEYNTALFKQETIERWKQYWMELLD 2504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-1995; E02349.
20-JUN-1994; EP-201761.
(UNIL.) UNILEVER NV.
(UNIL.) UNILEVER PLC.
De Vlieg J. Frenken LGJ, Peters H, St
Verrips CT;
                                             199 ----ELRYSVALVLKEMAELEKKCERKLOD
                                                                                                                                                                                                                                                                         Pseudomonas pseudoalcaligenes.
Key Location/Qualifiers
2440 NIKDL-----TMKGIQLEP
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                                                                                                                                                                   R88023 standard; protein; 289
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Best Local Similarity 25.9
Matches 49; Conservative
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Sequence:

Run on:

Searched:

Database

Result No.

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7.8%; Score 86.5; DB 2;
22.1%; Pred. No. 0.067;
tive 33; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL TUMORIGENESIS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
SOFTWARE: FastSED for Windows Version 2.0
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,260
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
PCT-US95-02792-2
US-08-188-228-44
US-08-332-638-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08822260
Patent No. 5830660
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drave
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 amino acids
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TOPOLOGY: lineal
IMMEDIATE SOURCE:
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TOPOLOGY: linear
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-822-260-1
LENGIH:
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Sequence 32, Appl
Sequence 32, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 92, Appl
Sequence 1, Appl
Sequence 18, Appl
Sequence 1, Appl
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Sequence 3, Appli
Sequence 11, Appli
Sequence 18, Appl
Sequence 37, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 20, Appli
Sequence 20, Appli
                                                                                                                                                                   May 15, 2000, 01:46:14 ; Search time 35.18 Seconds (without alignments) 92.094 Million cell updates/sec
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Patent No. 5290690
Patent No. 5290690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Appli
Sequence 19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MSALGAAAPYLHHPADSHSG.....ALVLKEMAELEKKCERKLQD 224
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Sequence 19,
Sequence 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143561
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                                Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-083-590A-18
US-08-046-128-37
US-08-0564-53-32
US-08-083-590A-11
US-08-08-083-590A-22
US-08-083-590A-20
US-08-530-950-6
US-08-530-950-6
US-08-530-950-10
US-08-530-950-6
US-08-530-950-6
US-08-530-950-6
US-08-530-950-8
US-08-64-136-92
US-08-64-136-92
US-08-64-136-18
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US-08-966-318-1
US-08-484-101B-36
US-08-484-101B-50
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US-08-221-817-19
US-08-454-439-19
PCT-US94-10487-19
US-08-317-4508-15
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                        143561 seqs, 14463640 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                            US-09-223-796-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 1000000
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Match Length
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Maximum DB seq
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779.5
779.5
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778.5
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778.5
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Perfect score:
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Gaps

47;

Length 195; Indels

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144 QQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQELRYS
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Best Local Similarity 23.5%; Pred. No. 1.1;
Matches 54; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GOLdstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3060000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           APPLICANT: Donahoe, Patricia K.
APPLICANT: Ragin, Richard C.
APPLICANT: MacLaughlin, David T.
TITLE OF INVENTION: Burification of
TITLE OF INVENTION: Substance
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                       204 VAL----VLKEMAELEKKCERKLQ 223
                                                                                                            170 CNMEQLQDLVGKLKDASKSLERATQ 194
                                                                                                                                                                                                     Sequence 1, Application US/07683957B
Patent No. 5310880
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
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US-07-683-957B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                                                                                                                                                141 VAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKL--TDGSAH---RFEVPIA 195
                                                                                                                                                                         81 RLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDS 140
                                  12 OMLADPRSFDSNAFTLLLRAAFQSLLDAQADEAVLDHPDLKHIDPVVLKHCHAAA----
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APPLICANT: Hillman, Jennifer L.
APPLICANT: GOll, Surya K.
TITLE OF INVENTION: NOVEL TUMORIGENESIS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Score 82.5; DB 2;
20.0%; Pred. No. 0.18;
iive 31; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FRASTEM: DOS
SOFTWARE: FRASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,260
CLASSIFICANTON THE FROM THE CLASSIFICATION TO SOFTET THE CLASSIFICANTON TO SOFTET THE CLASSIFICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive STATE: CA COUNTRY: USA ZIP.
 QLLKD---LDRSTFRKLLKLVVGALHGKDCREAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0247 US
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                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08822260 Patent No. 5830660
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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amino acid
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Best Local Similarity 20.0%
Matches 29; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLONE: 265569
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TOPOLOGY: 11r
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290 FLETLTRIVRALRVPARASAPRLALDPDAL-----AGFPQGLVNLSDPAALERLLDGE 343
230 LQALLFGDDHRCFTRMTPALLLLPRSEPAPLPAHGQLDTVPFPPPRPSAELEESPPSADP 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 PSPEVTAVAQLL---KDLDRSTFRKLLKLVV----GALHGKDCREAVEQLGASÅNLSEER 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| : : : : ||| 344 EPLLLLRPTAATTGDPAPLHDPTSAPWATALARRVAAELQAAAAELRSL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 560
                                                                                                                                                                                                                                                                                                                                                                                                                           of M llerian Inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURPLIEN. COMPUTER: PC-DOS/MS-DOS SOFTWARE: PATENTIN Relegase #1.0, Version #1.25 CURRENT APPLICATION DATA: US/07/683,957B FILING DATE: 19910412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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Sequence 32, Application US/08264534
Patent No. 5648464
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennle & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 --LQ-----ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.1%; Score 79.5; DB 2; Length 681;
28.9%; Pred, No. 2.7;
                                                                                            COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 ISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604 LPTSLPS-SLVPPVTAAQFLTPPSQHSYSSPV 634
                                                                                                                                                                                                                                                                     CLASSIFCATION: 530
PROOR APPLICATION DATA:
APPLICATION NUMBER: 07/879,038
FILING DATE: 30.ARR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 7326-009
TELEROMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 863864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/346,128 FILING DATE:
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Matches 44; Conservative
                                                                                                                                                                                      SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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; MOLECULE TYPE: peptide
US-08-346-128-37
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                  STATE: New York COUNTRY: U.S.A. ZIP: 10036
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: U.S.A.
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US-08-264-534-32
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STATE:
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                                                                                                            APPLICANT: Artavanis-Tsakonas, S. et al. TITLE OF INVENTION: Therapeutic And Diagnostic Methods TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And TITLE OF INVENTION: Nucleic Actids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 --LQ------ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Indels 15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: Z5-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%; Score 79.5; DB 28.9%; Pred. No. 2.7; tive 17; Mismatches
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                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STRET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: We York
COUNTRY: U.S.A.
                                         Sequence 18, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08346128
Patent No. 5856441
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTARION UNDBER: 18,872-
REFERENCE/LOCKET MUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 790-9090
TELEFAX: 212 869884/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 681 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 28.99
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                               COUNTRY: U
RESULT 4
US-08-083-590A-18
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us-09-223-796-2.rai

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GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Markavitch, Marc A.T.
APPLICANT: Feboo, Richard G.
APPLICANT: Rebay, Ilaria
APPLICANT: Blanumellar, Cristine M.
APPLICANT: Blanumellar, Cristine M.
APPLICANT: Blanumellar, Cristine M.
APPLICANT: Blanumellar, Cristine M.
APPLICANT: INPORTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   953 QSLQPPPPPPPPPHLGVSSAASGHLGR-SFLSGEPSQADV-QPLGPSSLAVHTILPQESPA 1010
                                                                                                                                                                                                                                                                                                                                                           55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 --LQ-----ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVA 162
                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 7.1%; Score 79.5; DB 1; Length 1078;
Best Local Similarity 28.9%; Pred. No. 5.5;
Matches 44; Conservative 17; Mismatches 76; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1011 LPTSLPS-SLVPPVTAAQFLTPPSQHSYSSPV 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: PENNIE & EDMONDS: 1155 Avenue of the Americas New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SED ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Sequence 32, Application US/08465500
; Patent No. 5789195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1078 amino acids TYPE: amino acid
TELEX: 66141 PENNIE | INFORMATION FOR SEQ ID NO: 11 SEQUENCE CHARACTERISTICS: LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-465-500-32
                                                                                                                            TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-083-590A-11
                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino a STRANDEDNESS:
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US-08-465-500-32
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US-08-083-590A-11

Sequence 11, Application US/08083590A

Sequence 11, Application US/08083590A

Patent No. 5786158

PATENTE OF INVENTION: Therapeutic And Diagnostic Methods

TITLE OF INVENTION: Therapeutic And Diagnostic Methods

TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

STREET: 1155 Avenue of the Americas

CONTESTATE: New YORK

STAFF: New YORK

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             893 MYGPLHSSLAASALSOMMSYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQ 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 --LQ------ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PACE COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/083,590A
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.1%; Score 79.5; DB Best Local Similarity 28.9%; Pred. No. 5.5; Matches 44; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAX-1991
ATTORNEY/AGENT INFORMATION:
        APPLICATION NUMBER: US/08/264,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18 872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPHONE: 212 869864/9741
                                                                                                                                                                           ALTURENT ACCUS.

NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
TELEFAX: 212 869884/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-264-534-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New )
COUNTRY: U.S
ZIP: 10036
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953 QSLQPPPPPPPPPLLGVSSAASGHLGR-SFLSGEPSQADV-QPLGPSSLAVHTILPQESPA 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79.5; Pred. No. 21;
                                                            1011 LPTSLPS-SLVPPVTAAQFLTPPSQHSYSSPV 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 25-JUN-1993
CLASSIFICATION: 425
ATTORNEY, AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,877
TELEFORMEROE/DOCKFT.
                                     163 ISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 ISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPI 194
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           Sequence 20, Application US/08083590A Patent No. 5786158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-530-950-6; Sequence 6, Application US/08530950; Patent No. 5736381; GENERAL INFORMATION:
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SED ID NO: 20:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%;
Best Local Similarity 28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-083-590A-20
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                     New York
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10036
                                                                                                                                      RESULT 10
US-08-083-590A-20
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Patent No. 585641
GENERAL INFORMATION:
APPLICANT: Attavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 585641ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
WMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                    113 --LQ-----ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVA 162
                                                                                             55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
                                                                                                                        113 --LQ-----ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1078;
                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                       16;
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                7.1%; Score 79.5; DB 1; 28.9%; Pred. No. 5.5;
                                                       44; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                 163 ISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879,038
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 28.9%
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-346-128-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            US-08-346-128-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                       Matches
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APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
MITTLE OF INVENTION: Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 MVGPLHSSLAASALSQMMSYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQ 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2407 OSLOPPPPPPPPPPPRGVSSAASGHLGR-SFLSGEPSQADV-QPLGPSSLAVHTILPQESPA 2464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 -- LQ-----ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590a
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ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
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Sequence 92, Application US/08874186
Patent No. 5989885
SERVEAL INFORMATION:
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Perry III, William L.
APPLICANT: Skolnick, Mark H.
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: 617/2000 TELERAX: 200154 TELEX: 200154 TELEX: 200156 TELEX: 200157 TELEX: 200157 TELEX: 200157 TELEX: 399 amino acids TYPE: amino acid STRANDEDNESS: not relevant "TOTO" Inear
                                                                                                                     TITLE OF INVENTION: CYTTITLE OF INVENTION: ONC TITLE OF INVENTION: KIN NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                             RY: USA
02110-2804
                                                                                                                                                                                                                                                          Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 ------PHVSYFRW------RVDVAISTSAQSRSLQPSVL--MQLKLTDG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 PD-----AFQEELQELGIPQDLIGDLASLAFGSQRPL----LDSVAQQQGSSL---- 150
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
ITILE OF INVENTION: CYTOKINE-, STRESS-, AND
ITILE OF INVENTION: ONCOPOTEIN-ACTIVATED HUMAN PROTEIN KINASE
ITILE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AQLLKDLD---RSTFRKLLKLVVGALHGK-D 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 78.5; DB 1; Length 363; Pred. No. 1.3; 41; Mismatches 94; Indels 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Indels
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IDAPPY disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: U9-SEP-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Fease, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 SAHRFEVPIAKFQELRYSVALVLKEMAELEKKC 218
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Sequence 10, Application US/08530950

Patent No. 5736381

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not relevant
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 363 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.1%;
Best Local Similarity 20.9%;
Matches 57; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Davis, Roger J. APPLICANT: Raingeaud, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 GRVSFLGSQPSPEVTAV---
                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-530-950-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      음
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232 PSNILLDRSGNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVW 291
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Gupta, Shashi
Derijard, Benoit
Vention: CYTOKINE-, STRESS-, AND
VENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
VENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 399,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIN SOLDEN.
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: U9-SEP-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Fease, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/01001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.1%; Score 78.5; D. Best Local Similarity 20.9%; Pred. No. 1.5; Matches 57; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 SAHRFEVPIAKFQELRYSVALVLKEMAELEKKC 218
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1136 VIGAASPVGDOLVRWLADRGAERLVL---AGACPGDDLLAAVEEAGAS-----AVVC 1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 VTAVA----QLLKDL-DRSTFRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVLL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1245 AVEREVYCSSVAGIWGGAGMAAYAAGS--AYLDALAEHHRARGRSCTSVAWTPW 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Ratingeaud, Joel
APPLICANT: Gupta, Jashi
APPLICANT: Gupta, Jashi
APPLICANT: Derijard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 77; DB 2; Length 3567;
25.3%; Pred. No. 66;
tive 23; Mismatches 45; Indels
                             NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS: 27 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Edward H. Gorman STREET: Abbort Laboratories D377/AP6D-2 One Abbott STREET: Park Rd CITY: Abbott Park
                                                                                                                                                                                      COUNTRY: 10

ZIP: 60064-3500

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-10/2/MS-DOS
SOFTWARE: PATENTIN PC-10/2/MS-DOS
SOFTWARE: PATENTIN RC-10/2/MS-DOS
SOFTWARE: PATENTIN RC-10/2/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-11
CLASSIFICATION: 435 4
ATONEX/AGENT INFORMATION:
NAME: DAUCKETS, ANDTERS MA
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 32652
REFERENCE/DOCKET NUMBER: 32652
TELEPRAK: 708-937-9396
            Erythromycin Analogs
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US-08-530-950-8
Sequence 8, Application US/08530950
; Patent No. 5736381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.35
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-642-734C-4
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ZIP: 02110-2804
COMPUTER READABLE FORM:
         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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STREET: 22.
"w: Boston
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                                                                                                                                                                        STATE:
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  SPECIFIC MUTATIONS OF MAP KINASE KINASE
4 (MKK4) IN HUMAN TUMOR CELL LINES IDENTIFY IT A.C. A TUMOR
SUPPRESSOR IN VARIOUS TYPES OF CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 PSNILLDRSGNIKLCDFGISGQLVDSIAKTRDAGCRPYMAPERIDPSASRQGYDVRSDVW 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 ------PHVSYFRW------RVDVAISTSAQSRSLQPSVL--MQLKLIDG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 SLGITLYELATGRFPYPKWNSVFDQLTQVVKGDPPQLSNSEBREFSPSFINFVNLCLIKD 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 GRVSFLGSQPSPEVTAV-----AQLLKDLD---RSTFRKLLKLVVGALHGK-D 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 78.5; DB 2; Length 399; 20.9%; Pred. No. 1.5;
Live 41; Mismatches 94; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/07642734C;
Patent No. 5824513
GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
                                                                                                                ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 STREET: Washington STATE: DC
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,186
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/782,482
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
RECISTATION NUMBER: 24884-121392-01
FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 SAHRFEVPIAKFQELRYSVALVLKEMAELEKKC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 ESKR----PKYKELLKHPFILMYEERAVEVAC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 amino acids amino acids
TITLE OF INVENTION: SPECTITLE OF INVENTION: 4 (MTITLE OF INVENTION: SUPPINDER OF SEQUENCES: 96 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       best Local Similarity 20.9
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-874-186-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 CREAVEQLGASAN--
                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 CWICMELMSTSFDKFYKYVYSVLDDVIPEEILGKITLATVKALMHLKENLKIIHRDIKPS 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.9%; Score 76.5; DB 1; Length 393; Best Local Similarity 21.4%; Pred. No. 2.5; Matches 58; Conservative 41; Mismatches 95; Indels 7
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
ATTONEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELEFOOKET UNBER: 0717/210001
TELEFAX: 617/542-5070
TELEFA
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Search completed: May 15, 2000, 03:22:30 Job time: 5776 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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search,
protein
1
protein
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May 15, 2000, 01:51:10 ; Search time 52.16 Seconds (without alignments) 251.784 Million cell updates/sec Run on:

US-09-223-796-2 Perfect score:

1 MSALGAAAPYLHHPADSHSG......ALVLKEMAELEKKCERKLQD 224 Sequence:

Scoring table:

168808 seqs, 58629743 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

168808 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

Database

pirl:*
pir3:*
pir4:* PIR_63:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			Sormanies	
Result No.	Score	Query	Length	DB	ID	ä
	104.5	4.6	676	7	S41022	hypothetical prote
7	93	8.4	486	~	D72007	Cr863 hypothetical
m	91	•	28	ч	139710	cellulose biosynth
4	89.5	•	43	N	T19632	hypothetical prote
'n	89		318	~	JC5837	0
φ	4	•	67	~	T00328	ന
7	84.5	7.6		~	T19780	
ထ	84.5	7.6	155	7	B71603	RESA-H3 antiqen PF
σ	84	7.6			T06981	low-molecular-weig
10	84	7.6			T06505	glutenin low molec
11	84	7.6			A55877	tumor necrosis fac
12	84	7.6			S67803	probable membrane
13	84	7.6	_		A55875	
14	84	7.6	4		T13734	- 13
15	•	•			T26189	
16	83.5	7.5	1583		T14176	ຜ
17	83	7.5	200		S72612	RNA helicase II -
18	æ	7.5	302		F69000	cobalamin biosynth
19	3	7.4	817		T03852	protein phosphatas
20	82.5	7.4	907		JG0193	G protein-coupled
21	82	7.4	260		WFHUM	mullerian inhibiti
22		7.3	734		E72271	5-methyltetrahydro
23	-	7.3	1354		T13363	phosphor1bosylform
24	81	7.3	459		T19347	hypothetical prote
25	81	7.3	1295		T24587	
56	80.5	7.2	315	~	I64065	acetyl-CoA carboxy
27	0	7.2	13	Н	GNMVRV	pol polyprotein -
28	80.5	7.2	1325	~	S16129	dynein-associated
29	80.5	7.2	33	~	A53824	nuclear pore membr
30	80.5	7.2	1479	7	T17401	transcription requ

talin - slime mold hypothetical prote	transcription fact exonuclease (EC 3.	DNA-binding protei peptide synthetase	surfactin syntheta	probable anthranil	hypothetical prote	pol polyprotein -	pol polyprotein -	1-phosphatidylinos	beta-galactosidase	notch protein homo	hypothetical prote
A57036 T04861	A45580 BVECSC	S52863 C69681	I40485	T35072	C72761	GNVWK	GNMVGV	S65741	JS0610	A40043	T28697
00	~ ~	~	7	7	7	Н	Н		7	7	~
2491 368	998 1048	1324	3588	502	694	843	1196	1466	1928	2555	431
7.2	7.2	2.7	7.2	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1
80.5	8 8 80	8 80 80	80	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79
31	33 34	32 36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

S41022 hypothetical protein T07C4.9 - Caenorhabditis elegans

Upporterized process: Caenorhabditis elegqns C; Species: Caenorhabditis elegqns C; Species: Caenorhabditis elegqns C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997 C; Accession: \$41022

R; Berks, M.
submitted to the EMBL Data Library, January 1994
A; Reference number: \$41014
A; Reference number: \$41014
A; Reference number: \$41014
A; Residues: 1-676 < CBER
A; Molecule type: DNA
A; Residues: 1-676 < CBER
A; Cross-references: EMBL: 229443; NID: 91067051; PID: 9443836
C; Genetics:
A: Introns: 69/3; 161/1; 208/3; 227/1; 357/1; 505/3
C; Superfamily: annexin repeat homology < Axis
F; 373-444 Domain: annexin repeat homology < Axis
F; 528-600/Domain: annexin repeat homology < Axis
F; 528-600/Domain: annexin repeat homology < Axis

49; 676; Length Indels Query Match
9.4%; Score 104.5; DB 2;
Best Local Similarity 25.7%; Pred. No. 0.88;
Matches 47; Conservative 34; Mismatches 53;

10;

----QRPLLDSVAQ 143 43 LDRSTFRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLP 100 90 50 INNSKFRKILCELV-----KESR------SHEMISEBOLATLYDCATTSTRL----101 PASLKPDAFQEELQELGIPQDLI--GDL--ASLAFGS----g δ

144 QQ-GSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQELRY 202 요 ò

g

203 SVA 205 ò

201 QLA 203

g

RESULT D72007

CT863 hypothetical protein - Chlamydia pneumoniae (strain CWL029)
C;Species: Chlamydia pneumoniae
C;Species: Chlamydia pneumoniae
C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 08-Oct-1999
C;Accession: D7207;
C;Accession: D7207;
C;Accession: D7207;
Natchan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.

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156 RWRVDVAI-STSAQSRSLQPSVLMQLKLTDGS
                                                                                                                                                                                                                                                                                                         1-433 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: C32A3.3
A; Map position: 3
                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 57;
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                             A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-486 cARN>
A:Cross-references: GB:AE001682; GB:AE001363; NID:g4377344; PIDN:AAD19159.1; PID:g437735
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: CPn1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cellulose biosynthesis protein celD - Agrobacterium tumefaciens
Cellulose biosynthesis protein celD - Agrobacterium tumefaciens
Cilate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: 139710
R;Matthyse, A.G.; White, S.; Lightfoot, R.
J; Bacteriol. 177, 1069-1075, 1995
A;Title: Genes required for cellulose synthesis in Agrobacterium tumefaciens.
A;Reference number: 139709; MUID:95164506
A;Reference number: 139709; MUID:95164506
A;Residues: 1-584 < RES.
A;Roccasion: 139710
A;Residues: 1-584 < RES.
A;Residues: 1-584 < RES.
A;Cross references: GB:L38609; NID:9710486; PIDN:AAC41431.1; PID:9710488
C;Comment: This protein is required for cellulose biosynthesis.
C;Genetics:
A;Genetics:
C;Superfamily: Agrobacterium tumefaciens cellulose biosynthesis protein celD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFR------WRVDVAI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 Q-----HILLQQALRIPP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 QGFKTYDFLRGNEPYKYFFGPEEHKLSCTLFRTRSGDNLGGTLHPRSVRFVYEQALKLYK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ASLKPDAFQ-EELQ 114
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    27 SQPSPEVTAVAQLLKDLDRSTFRK---LLKLVVG-----ALHGKDCREAVEQLGASAN 76
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                                                                                                                                                                                                                                                                                                NMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSSSTDALISLALGQI
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8.2%; Score 91; DB 1; Length 584;
Best Local Similarity 25.0%; Pred. No. 8.8;
Matches 53; Conservative 27; Mismatches 76; Indels
                                                                                                                                                                                                 DB 2; Length 486;
                                                                                                                                                                                             8.4%; Score 93; DB 2; Length 486
21.9%; Pred. No. 4.8;
tive 35; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 VSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVG-
                                                                                                                                                                                                                                                                                                                                         LSEERLAVLLAGTHTLLQQALRLPP-----
A; Reference number: A72000; MUID: 99206606
A; Accession: D72007
                                                                                                                                                                                                                                 54; Conservative
                                                                                                                                                                                                              Local Similarity
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234 ERDQDRQ 240
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Best Local S:
Matches 54,
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C; Species: Rattus norvegicus (Norvay rat).
C; Date: 05-War-1998 #sequence_revision 13-Mar-1998 #text_change 20-Aug-1999
C; Accession: JC5837
R; Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y.
Cell Struct. Funct. 22, 565-577, 1997
A; Title: Identification and characterization of rat 364-kDa Golgi-associated protein A; Reference number: JC5837; MUID: 98093490
A; Reference nucleic acid sequence not shown
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CESP: C32A3.3
                                                                                                                                                                                                                                                                                                                                            hypothetical protein C32A3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T19632; T19975
R;Thomas, K. submitted to the EMBL Data Library, February 1995
A;Reference number: Z19154
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 FEEELEQVEKTYRKDIDDLQQMVKSLVNENRNLSTTV----SSLPN-----HADSPVS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSAQSRSLQPSVLMQLKLTDGSAHRFEVPI-----AKFQELRYSVALVLKEMAELE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || : |: :|::|| | : |: TSMREADLK--MLLELK-EMSSQQRDEIKALQKDVDTYQCQVENLQNSIEKLIRQNEELL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 HGKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPA--SLKPDAFQEELQELG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AAAPYLHHPADSHSGRVSFLGSQ-----PSPEVTAVAQLLKDLDRSTFRKLLKLVVGAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 IPQDL-----IGDLASLA---FGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:248241; PIDN:CAA88286.1; GSPDB:GN00021; A;Experimental source: clone C32A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Burton, J.
submitted to the EMBL Data Library, November 1996
A;Reference number: 219206
A;Accession: 119975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-433 <WIZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 61/3; 94/3; 191/1; 229/3; 298/3; 356/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 23.6%; Score 89.5; DF Similarity 23.6%; Pred. No. 7.9; 77; Conservative 39; Mismatches
434 GWRIGETLRCATALSRASEPSQVINVRVPPGS 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364K Golgi complex-associated protein - rat
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Gaps

55;

--ELEKKCER 220

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A;Residues: 1-1558 <GAR>
A;Cross-references: GB:AE001424; GB:AE001362; NID:g3845307; PID:g3845309; TIGR:PFB091
A;Cross-references: GB:AE001424; GB:AE001362; NID:g3845307; PID:g3845309; TIGR:PFB0915A
C;Genetics:
A;Gene: PFB0915w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A) Reference number: A71600; MUID:99021743
A) Accession: B71603
                                                                                                                                                                                                    A;Residues: 1-674 <WIL>
A;Cross-references: EMBL:280215; PIDN:CAB02274.1; GSPDB:GN00019; CESP:C36B1.9
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  C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19780
C;Accession: T19780
Submitted to the EMBL Data Library, September 1996
A;Accession: T19780
A;Accession: T19780
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESA-H3 antigen PFB0915w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999
C;Accession: B71603
R;Gardner, M.J.; Tettelln, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; R.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELG--IPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----IRLRGKRDKTSIRPSVV--- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----HRYDSEFKKIDEVERSMNRVLHNVIKLQSGETLPRPAPTITIPYWQLDREYRR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVLL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1558;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 674;
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                                                                                                                                                                                                                                                                                                                                                                                                            7.6%; Score 84.5; Di
21.2%; Pred. No. 35;
tive 30; Mismatches
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s; Pred. No. 99;
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 --IADLVNLTMGELYEHLKAVFNA----
                                                                                                                                                                                                                                                                                                                     A;Map position: 1
A;Introns: 131/1; 179/1; 266/3; 468/2
                                                                                                                                                                                                                                                      A; Experimental source: clone C36Bl
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21.6%;
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Best Local Similarity 21.6%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 21.2%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                A; Gene: CESP: C36B1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 KLQD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein KIAA0552 - human
C;Species: Homo sapiens (man)
C;Accession: T00328
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
B;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Reference number: 214086; MUID:98290545
A;Reference number: Ishikawa, A;Nabolcule type: mRNA
A;Nabolcule type: mRNA
A;Nabolcule type: mRNA
A;References: EMBL:AB011124; NID:d1185394; PIDN:BAA25478.1; PID:d1026408
A;Cross-references: EMBL:AB01124; NID:d185394; PIDN:BAA25478.1; PID:d1026408
A;Note: KIAA0552
A:Residues: 1-3187 <TOK>
A:Residues: 1-3187 <TOK>
A:Cross-references: DBB1.225543; NID:9516825; PIDN:BAA05026.1; PID:d1005567; PID:9516826
C;Comment: This protein plays a role in the formation and maintenance of the characteris C;Superfamily: giantin
E:40-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status predict F;3165-3187/Domain: membrane anchor #status predicted <MAD>
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                                                                                                                                                                                                                                                                                              1277 LLLQEQINEQGLEI------QNLKAASHEAKAHTEQLKQELESSQLKIADLEHL 1324
                                                                                                                                                                                                                                                                                                                                                           LGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEEL-QELGIPQDLIGDLASL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSSMGRPGHLGSGEGGGGLPFAACSPPSP----SALIQELEERLMEK--EQEVAAL- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 -ELQELGIPQD--LIGDLASLAFGSQRPLLDSVA---QQQGSSLPHVSYFRWRV----D 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| | : || : || : || : || || 389 LQLQVLRLQQDKKQLQEEARKMRQKEELEDKVAACQKEQADFLPRIEETKWEVCQKAGE 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKDCREAVEQLGAS-ANLSEER-----LAVLLAGTHTLLQQALRLPPASLKPDAFQE- 112
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                                                                                                                                                                                                                                                                    LHHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALHGKDCREAVEQ 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                             130 AFGSQRPLLDSVAQQQGSSLPHVSYF-----RWRVDVAISTSAQS-----RSLQPSVLM
                                                                                                                                                                                                                              34;
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                                                                                                                                                                               Length 3187;
                                                                                                                                                                           Query Match 8.0%; Score 89; DB 2; Length 318 Best Local Similarity 21.8%; Pred. No. 1.1e+02; Matches 49; Conservative 47; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1383 QAKEHEERLKQVQVEICELKKQPKE----LEEESKAKQQLQRKLQ 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 QLKLTDGSAHRFEVPIAKFQELRYSVALVLKEMAELEKKCERKLQ 223
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hypothetical protein C36B1.9 - Caenorhabditis elegans
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Pred. No. 35
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Matches 54; Conservative
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O.; Smith,

10;

Gaps

65;

Mon May 15 14:56:35 2000

DD 1049 AKDDTLEKVIEEEHDITTTLDEVVELKDVEEDKIEKVSDLKDLEEDILKEVKEIKELESE 1108	Query Match Best Local Sim
Qy 182LTDGSAHRFEVPIAKFQELRYSVALVLKEWAELEKKCERKLQ 223	Matches
1109 II	07 39 LEFA- 111 Db 38 LPPQOS
UY 224 D 224	Ov 153 SYFRWR
Db 1169 E 1169	96
RESULT 9	Qy 205 ALVLKE
low-molecular-weight glutenin storage protein - wheat C. Species: Trittum aestivum (common wheat)	Db 156 MWQQSS
C.bace. Jo Apr. 1959 *Bequence_revision Jo Apr. 1959 *Lext_change Zo Ang 1959 C.Accession. 106981	RESULT 11 A55877
submitted to the EMBL Data Library, January 1997 A:Reference number: 215843	tumor necrosis C; Species: Homo
A;Accession: Tubski A;Status: preliminary: translated from GB/EMBL/DDBJ A:Molecule type: mRNA	C;Date: 23-Mar-1 C;Accession: A55 R;Song, H.Y.: Du
A;Residues: 1-303 <and> A;Cross-references: EMBL:U86028; NID:q1857655; PIDN:AAB48477.1; PID:q1857656</and>	J. Biol. Chem. 7 A; Title: Identif
A; Experimental source: cv. Cheyenne C; Genetics:	A; Reference numb A; Accession: A55
A:Map position: 1 C:Function:	A;Status: prelin A;Molecule type:
A;Description: seed storage protein in the endosperm C:Superfamily: gliadin C:Kevwords: seed: storage protein	A; Residues: 1-66 A; Cross-referenc
Query Match 7.6%; Score 84; DB 2; Length 303; Best Local Similarity 27.3%; Pred. No. 14; Matches 38; Conservative 18; Mismatches 67; Indels 16; Gaps 4;	Query Match Best Local Sim Matches 46;
Qy 99 LPPASLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHV 152	Qy 49 RKLLKI
PFSQQQQPLPQQPSFSQQQPPFSQ	DD 80 KKLLDI
QY 153 SYFRWRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQELRYSV 204	Qy 108 AFQEE-
Db 96 ŚPFSQQQQLVLPPQQQQQLVQQQIPIVQPSVLQQLNPCKVFLQQQCSPVAMPQRLARSQ 155	Db 132 INAEKG
OY 205 ALVLKEMAELEKKCERKLQ 223	Qy 157 WRVDVA
Db 156 MWQQSSCHVMQQQCCQQLQ 174	Db 192 SAFMVA
RESULT 10	Qy 217 KC
r06505 glutenin low molecular weight chain precursor (B-I) - wheat	Db 245 DCKEFS
C; Species: IIILICum destrivum (common wheat) C; Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 12-Nov-1999	RESULT 12
R,Okita, T.W.; Cheesbrough, V.; Reeves, C.D.	so/803 probable membran
J. Biol. Chem. 260, 8203-8213, 1985 Aritie: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA s A:Reference number: A92541: MUTD:8524522	N;Alternate name C;Species: Sacch
A; Accession: T05505 A; Status: preliminary: translated from GR/FMRL/DDRI	C, Accession: S67
A. Molecule type: mRNA A. Poseiding: 1-304 / 0001	submitted to the
A: Acsistates: 1.50% Construction of the const	A; Reletence numer A; Accession: S67
C: Keywords: seed; storage protein F:1-23/Domain: storage sequence #status predicted <sig></sig>	A:Cross-reference
F;24-304/Product: glutenin low molecular weight chain (B-I) *status predicted <mai></mai>	A; Experimental s C; Genetics:

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Dunbar, J.D.; Zhang, Y.X.; Guo, D.; Donner, D.B. 1574-3581, 1995
11f.cation of a protein with homology to hsp90 that binds the type 1 tum iber: A55877; MUID:95181307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e: DNA
790 <ALITA
nces: EMBL:274287; NID:91431405; PID:e253369; PID:91431406; GSPDB:GN000
source: strain $288C
                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ane protein YDL239c - yeast (Saccharomyces cerevisiae)
mes: hypothetical protein D0771
charomyces cerevisiae
-1996 #sequence_revision 12-Jul-1996 #text_change 29-Oct-1999
67803
                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens (man)
1995 #sequence_revision 23-Mar-1995 #text_change 05-Nov-1999
                                                                                                                                                                                           --SLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDS---VAQQQGSSLPHV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVVGALHGKDCREA-VEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LQELGI----PQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSY----FR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQELRYSVALVLKEMAELEK 216
                                                                                                                                                                 RVDVAISTSAQSRSL------QPSVLMQLKLTDGSAHRFEVPIAKFÖELRYSV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Gaps
                                                                                                          16; Gaps
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e: mRNA
661 <SON>
nces: GB:U12595; NID:g687236; PIDN:AAA87704.1; PID:g687237
heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                               factor type 1 receptor associated protein TRAP-1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%; Score 84; DB 2; Length 661;
lmilarity 23.8%; Pred..No. 37;
Conservative 39; Mismatches 76; Indels
7.6%; Score 84; DB 2; Length 304;
larity 27.3%; Pred. No. 14;
Conservative 18; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.; Schneider, C.; Moro, M.
He Protein Sequence Database, July 1996
uber: S67798
                                                                                                                                                                                                                                                    EMAELEKKCERKLQ 223
                                                                                                                                                                                                                                                                              SCHVMQQQCCQQLQ 174
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                     milarity
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A;Gene: MIPS:YDL239c
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hypothetical protein W05B5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26189
R;McLay, K.
submitted to the EMBL Data Library, November 1996
A;Reference number: 220167
A;Accession: T26189
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-336 <WIL>
A;Cross references: EMBL:282071; NID:e1298254; PIDN:CAB04919.1; GSPDB:GN00019; CESP:W
A;Experimental source: clone W05B5
                                                                                            groovin gene protein - fruit fly (Drosophila melanogaster) (fragment)
C; Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C; Accession: 113734
R; Strumpf, D.; Volk, T.
J. Cell Biol. 143, 1259-1270, 1998
A; Title: Kakapo, a novel cytoskeletal-associated protein is essential for the restric A; Reference number: 217746
A; Reference number: 217746
A; Reference number: 217746
A; Reference number: 217746
A; Reference number: 217746
A; Reference number: 217746
A; Reference number: 217746
A; Residues: 113734
A; Residues: 1-4151 <STR>
A; Coss. references: EMBL: V09430; NID:e1372000; PID:e1372001; PIDN:CAA70581.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2490 EHKPLLDKLNKTGEALGALVADDDGAKINEILDTDNARYAALRLELERERQQALESALQES 2549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 NLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQDLIGDLASLAFGS-Q 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AAAPYLHHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLK-----LVVGALH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 RPLLDSVAQQQGSSLPHVSYFRWRV-----DVAISTSAQSRSL-----QP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------AVAQ1LKDLDRSTFRKLL----KLVVGALHGKDCREAVEQLGASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 -SVLMQLKLTDGSAHRFEVPIAK------FQELRYSVALVLKEMAELEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 84; DB 2; Length 415
19.1%; Pred. No. 3.7e+02;
vative 51; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSALGAAAPYLHHPADSHSGRVSFLG-----SQPS---PEVT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
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24.8%; Pred. No. 17;
tive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:W05B5.3
A;Map position: 1
A;Introns: 5/1; 59/3; 109/3; 233/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.8%
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: grv
A,Map position: 2
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Best Local Simi
Matches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
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*Xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans
Nylternate names: purine hydroxylase I
C; Alternate names: purine hydroxylase I
C; Species: Emericella nidulans, Aspergillus nidulans
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A55875; A9819
R; Glattigny, A.; Scazzocchlo, C.
J. Biol. Chem. 270, 3534-3550, 1995
A; Title: Cloning and molecular characterization of hxA, the gene coding for the xanthine
A; Reference number: A55875; MUID:95181302
A; Accession: A55875
A; Molecule type: DNA
A; Residues: 1-1363 < GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 83/3; 151/3; 803/2
C:Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-2S] homology
C:Keywords: 2Fe-2S; FAD; flavoprotein; iron-sulfur protein; metalloprotein; molybdenum;
F;57-104/Domain: ferredoxin [2Fe-2S] homology <FERIX
F;73,78,81,103/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                          LQQALRLPPA--SLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PSTELNFETVGKSFP 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-1363 <GLA>
A;Cross-references: EMBL:X82827; NID:9577730; PIDN:CAA58034.1; PID:9577731
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 HITKEKYDSLGLDILTDLTYVQSQNLIKNLLIVL-------DIPLKTFLKIVPTIVI 726
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                         11 LHHPADSHSGRVSFLGSQPSPEVTAVAQL-----LKDLDRSTFRKLLKLVVGAL-- 60
                                                                                                                                                                                                                                                                                                                     60 -----SEERLAVLLAGKDCREAVEQLGASANL------SEERLAVLLAGTHTL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                       574 SEKIQKNAEDKLNDYMNEHQEIVEKLQNQALIASRWSTQIQESENTHKKITDELAGKQS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVS---YFRWRVDVAIS-TSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.6%; Score 84; DB 1; Length 1363; Best Local Similarity 22.5%; Pred. No. 92; Matches 46; Conservative 35; Mismatches 81; Indels
                                                                                                                        Length 790;
                                                predicted <TMM>
                                                                                                                                                                        86;
                                                                                                                          5;
                                                                                                                        Score 84; DB; Pred. No. 46; 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EILKLEETILSLKEDVFQEKLN----LKKLYGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELRYSVALVLKEMAELEKKCERKLQD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4L
C;Keywords: transmembrane protein
F;706-722/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---KFKOMRYGASVYLGDLAELRO 326
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                                                                                                                     Query Match 7.6%;
Best Local Similarity 21.4%;
Matches 57; Conservative 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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78;

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Indels

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150 PHYSYFRWRYDVAISTSAQSRSLQPS 175
                                          306 PHV---RHQVKRDVDSDEQLEEMKVS 328
               Dp
                        δ
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9
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Search completed: May 15, 2000, 03:23:35 Job time: 5545 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 15, 2000, 02:06:10 ; Search time 44.1 Seconds (without alignments) 154.692 Million cell updates/sec Run on:

US-09-223-796-2 1112 1 MSALGAAAPYLHHPADSHSG......ALVLKEMAELEKKCERKLQD 224 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

83857 segs, 30454973 residues Searched:

83857 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		de			SUMMARIES		
Result		Query					
Š.	Score	Match	Length	四 :	QI	Description	ption
1	84.5		673	1	Y552_HUMAN	060299	homo sapien
7	4		890	Н	RB6K_HUMAN	095235	рошо
e	84		304	Н	GDB1_WHEAT	P04729	triti
. 7	84		661	Н	TRAL_HUMAN	012931	homo sap
S	84		1363	Н	XDH_EMENI	012553	emeri
9	83		302	۳H	COBK_METTH	027083	_
7		•	260	Н	MIS_HUMAN	P03971	-
æ	81.5	7.3	1354	Н	PUR4_DROME	P35421	drosc
6	0		315	-	ACCA_HAEIN	P43872	
10	0		1196	Н	POL_MLVRD	P11227	
11	0		1280	Н	DYNA_RAT	P28023	
12	0	•	1337	Н	P152_YEAST	P39685	
13	0		2491	-1	TALA_DICDI	P54633	dictyosteli
14	80	•	314	-	IUNH_CRIFA	027546	crithidia f
15	80		887	Н	RB6K_MOUSE	P97329	
16	.08	7.2	1048		SBCC_ECOLI	P13458	
17	80		2555	-	PPS3_BACSU	P39847	
18	79.5		572	~1	PRIM_STAAU	005338	
19	79.5	7.1	843	-	POL_MLVAK	P03357	
50	79.5	•	1196	Н	POL_MLVAV	P03356	akv
21	79.5	7.1	1928	Н	LPH_RAT	002401	ratt
. 22	79	٠	1194	1	BCHH_RHOCA	P26162	
23		•	1270	-	DYNA_HUMAN	014203	
24	∞ .	•	397		MPK4_MOUSE	P47809	m dual spec
25	∞ .		399	~4	MPK4_HUMAN	P45985	
26	ထာ		791	1		045388	bordetella
27	78.5	٠	1281	Н	DYNA_MOUSE	008788	
28	œ	٠	1427		REST_HUMAN	P30622	
29	78		405	_	FLIK_SALTY	P26416	salmonella
30	78		1959	~	- 1	P14105	
31	- 1	٠	3587	-	SRF1_BACSU	P27206	bacillus su
32	_	٠	487	-1	AMPL_BOVIN	P00727	gog
ю (77.5	•	799		CAD8_MOUSE	P97291	mus muscu
34	_		362	Н	IF3A_MAIZE	Q9xhr2	zea mays (n

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15 ADSHSGRVSFLG-----SQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALH 60

P74996 zymomonas m P21146 bos taurus P06531 emericella P12845 caenorhabdi Q03132 saccharopol Q51152 nelsseria m P26809 friend muri Q22307 caenorhabdi Q07703 bordetella P25098 homo sapien P34314 caenorhabdi	ate) pdate) vertebrata; Mammalia; ae; Homo. Tanaka A., Kotani H., clones from brain which can matics and the EMBL outstation There are no restrictions on its may as its content is in no way ved. Usage by and for commercial See http://www.isb-sib.ch/announce/	67; Indels 59; Gaps 12;
4 1 GRP_ZYMMO 9 1 ARKI_BOVIN 8 1 TRPG_EMENI 7 1 MYSC_CAEEL 7 1 YGF_NEIME 4 1 POL_MLVFF 1 1 DDX9_CAEEL 1 1 DDX9_CAEEL 9 1 METC_BORAV 9 4 ARKI_HUWAN 1 1 YKT3_CAEEL	PRT; 673 As ed; ed; sequence update annotation upda; 52. craniata; Ve; ini; Hominidae; ini; Ho	28; 9
5 77 6.9 164 77 6.9 768 77 6.9 1947 8 77 6.9 3567 9 76.5 6.9 3267 1 76.5 6.9 1204 1 76.5 6.9 1301 2 76.5 6.8 1331 7 6 6.8 8395 7 6 6.8 68	1 552 HUMAN 552 HUMAN 60299; 5-JUL-1999 (Rel. 38 5-FEB-2000 (Rel. 38 5-FEB-2000 (Rel. 38 5-FEB-2000 (Rel. 38 1AAO552. IAAO552. IAAO552. IAAO554. IAAO564. IAAO564	Local Similarity nes 54; Conservat
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Q12931; 075235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local S1m
Matches 38;
                                                                                                                                                                                                                                                                                                                 GDB1_WHEAT
P04729:
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TRAL_HUMAN
                                                                                                                                                                                                                                                                                             GDB1_WHEAT
  633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3d 93:3418-3431(1999).
PUNCTION: INTERACTS WITH GUANOSINE TRIPHOSPHATE (GTP)-BOUND FORMS OF RABG. MAY ACT AS A MOTOR REQUIRED FOR THE RETROGRADE RAB-6
REGULATED TRANSPORT OF GOLGI MEMBRANES AND ASSOCIATED VESICLES
ALONG MICROTUBLES. HAS A MICROTUBULE PLUS END-DIRECTED MOTILITY
389 LQLQVLRLQQDKKQLQEEAARLMRQREELEDKVAACQKEQADFLPRIEETKWEVCQKAGE 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 99252096.
Horrevoets A.J.G., Fontijn R.D., van Zonneveld A.J., de Vries C.J.M.,
ten Cate J.W., Pannekoek H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDSVA-QQQGSSLPHVSYFRWRVDVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ALHGKD--CREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPAS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; FALSE_NEG.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOR protein; Microtubules; ATP-binding; Coiled coil; Golgi stack; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ten Cate J.W., Pannekoek H.; Wassular endochellal genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573 LLLKERQEKLQLEMHLRDEICNEMVEQMQQREQMCSEHLDTQKELLEEMYEEKLNILKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                                     15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
RABKINESIN-6 (RAB6-INTERACTING KINESIN-LIKE PROTEIN) (GG10_2).
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: GOLGI (BY SIMILARITY).
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98; Indels
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COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
7; 6620264615496051 CRC64;
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                                                                      161 VAI-----STSAQSRSLQPSVLMQLKLTDGSA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-ENDOTHELIAL CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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167
762
890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                          RBGK_HUMAN

AC 095235;
DT 15-FEB-2000
DT 15-FEB-2000
DT 15-FEB-2000
DT 15-FEB-2000
DT 15-FEB-2000
DE RABKINESIN-6
GN RABGKIFL.
OS HOMO SAPLINE;
992
RA HOLLINE; 992
RA HOLLINE; 992
RA HOLLINE; 993
RA HOLLINE; PR
CC HOLLINE; PR
CC HOLLINES FR
CC HOLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682 ASASTQOLQEVKAKLQQCKARLNSTTEELHKYQKMLEPPPSAKPFTIDVDKKLEEGQKNI 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPPA---SLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDS---VAQQQGSSLPHV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPFSQQQQLVLPPQQQQQLVQQQIPIVQPSVLQQLNPCKVFLQQQCSPVAMPQRLARSQ 155
                                                      163 ISTSAQSRSLQPSVLMQLKL----TDGSAHRFEVPI-------AKFQELRYSV 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
Poaceae; Trittcum,
L-TSFYQEEIQE----RDEKIEELEALL---QEARQQSVAHQQSGSELA----LRRSQRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67; Indels | 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAMMA-GLIADIN B-I.
807EBF447A59D6D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-UL-1999 (Rel. 38, Last annotation update)
GAMMA-GLIADIN B-I PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 84; DB 1
27.3%; Pred. No. 6.4;
lve 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            304 AA.
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                                                                                                                                                                                                                      762
                                                                                                                                                               205 ALVLKEMAEL-----EKKC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34252 MW;
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                                                                                                                                                                                                                742 RLLRTELOKIGESLOSAERAC
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                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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COBK_METTH
O27083;
15-JUL-1998 (
15-JUL-1998 (
15-JUL-1998 (
                                                                                                          STRAIN-BIA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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COBK_METTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AFQEE----LQELGI---PQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSY---FR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 WRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQELRYSVALVLKEMAELEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 SAFMVADRVEVYSRSAAAPGSLGYQWLSDGSG-VFE--IAEASGVRTGTKIII----HLKS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 RKLLKLVVGALHGKDCREA-VEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 TNAEKGTITIODIGIGMTQEELVSNLGTIARSGSKAFLDALQNQAEASSKIIGQFGVGFY 191
                                                                                                                                                                                           SEQUENCE OF 16-631 FROM N.A.
Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E., Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S., Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S., Ueng S., Tatum O., Campbell C., Fawcett J., Maltbie M., Misra M.,
                                                                                                                                          Song H.Y., Dunbar J.D., Zhang Y.X., Guo D., Donner D.B.; Infantification of a protein with homology to hsp90 that binds the type 1 tumor necrosis factor receptor."; J. Biol. Chem. 270:3574-3581(1995).
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-FBB-2000 (Rel. 39, Last annotation update)
TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN (TRAP-1)
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%; Score 84; DB 1; Length 661;
23.8%; Pred. No. 17;
tive 39; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EF527B93965032E5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00298; HSP90; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XDH_EMENI STANDARD;
Q12553;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U12595; AAA87704.1;
EMBL; AC005203; AAC24722.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 23.8%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 KC----ERKLOD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 :::|
245 DCKEFSSEARVRD
                                                                                                                   FROM N.A.
95181307.
                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 RLAVLLAGTHTLLQQALRLPPASLK-----PDAFQEELQ-ELGIPQDL-IGDLASLAFGS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 K-----GINGCCKGSSEET@EDVKHKFASPDFIEYKPDTELIFPPSLWKHELRPLAFGN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 KRK-----KLIGGSTETQIEI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -: SUBCELLULAR LOCATION PERCYISOMAL.
-: SUBCELLULAR LOCATION PERCYISOMAL.
-: SIMILARITY: TO OTHER XANTHINE DEHYDROGENASES, AND LIMITED TO OTHER ENTRARVOTIC MOLYBDOPTERIN ENZYMES SUCH AS NITRATE REDUCTASE AND SULFITE OXIDASE.
-: SIMILARITY: TO 2FE-2S FERREDOXINS IN THE N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 SFLGSQPSPEVTAVAQLLK-DLDRST-FRKLLKLVVGALHGKDCREAVEQLGASANLSEE 80
                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
71 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
749504 MW; P9464E66C22ACD97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         nidulans.";
J. Biol. Chem. 270:3534-3550(1995).
-!- CATALYTIC ACTIVITY: XANTHINE + NAD(+) + H(2)O = URATE + NADH.
-!- COFACTOR: FAD, MOUTUBOPPERIN, AND TWO 2FE-2S CLUSTERS.
                                                                                                                                                                                                                                                                                                                                                       Glatigny A., Scazzocchio C.; "Cloning and molecular characterization of hxA, the gene coding ithe xanthine dehydrogenase (purine hydroxylase I) of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF01315; Ald_Xan_dh_C; 1.
Oxidoreductase; NAD; Molybdenum; Flavoprotein; FAD; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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                                                                   HYDROXYLASE
                                                                                                                                                                   Eurotiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X82827; CAA58034.1; -
PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
PROSITE; PS00559; MOLYBODPTERIN_EUK; FALSE_NEG.
PRAM; PF00941; dehydrog_molyb; 1.
PFAM; PF01315; Ald_Xan_dh_C; 1.
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
XANTHINE DEHYDROGENASE (EC 1.1.1.204) (PURINE
                                                                                                                          Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Plectomycetes;
Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 ---KFKQMRYGASVYLGDLAELRQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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78
81
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78
81
81
1363 AA;
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DISULFID
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    MEDLINE; 98037514.

MEDLINE; 98037514.

MEDLINE; 98037514.

MAINTER, DOUGETEE-Stamm L.A., Deloughery C., Lee H.-M., Dubols J., Andredge T., Bashirzadeh R., Blakely D., Cock M., Gilbert R.,

Harrison D., Hoang L., Keagle P., Lumm W., Pothler B., Olu D.,

Mani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

McDougall S., Shimer G., Man J.-I., Rice P., Nolling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum
"Complete genome sequence of Methanobacterium thermoautotrophicum
"Tomplete Salvaryzes THE REDUCTION OF THE MACROCYCLE OF PRECORRIN-
"Tomplete Salvaryzes THE REDUCTION OF THE MACROCYCLE OF PRECORRIN-
"Tomplete Salvaryzes THE REDUCTION OF THE MACROCYCLE OF PRECORRIN-
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"Tomplete Salvaryzes THE REDUCTION OF THE MACROCYCLE OF PRECO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIS_HUMAN STANDARD; PRT; 560 AA.
P03971; 075246;
23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MUELLERIAN INHIBITING FACTOR PRECURSOR (MIS) (ANTI-MUELLERIAN HORMONE)
(AMH)_(MULLERIAN INHIBITING SUBSTANCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 -CILIDATHPFAAQATENALRACRETGTIYVRFERPEVIPDGVIRVGSFRE----- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 ISRLSGMPWVEVTATATTEHGSDLAEKSGASRTVTGALDSDGLRELMADLDA----- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 LAVLLAGTHTLLQQ----ALR-------LPPASLKPDAFQEELQELGIPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 -- AGEVASSLIGDGEVVMHLAGVSTLGDVLRSLEPERVAVRVLPSTSSIEKCLQLGVPPS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DLIGDLASLAFGSQRPLLD-SVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQ----PS
                                                           Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 VLMQLKLTDGSAHRF--EVPIAKFQELRYSVALVLKEMAE---LEKKCE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 HIIAMQ-----GRFSAEMNLALLREYR-AGAVITKESGETGGLPEKVE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.5%; Score 83; DB 1; Length 302;
24.5%; Pred. No. 7.6;
ive 30; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ase; NADP; Cobalamin biosynthesis.
302 AA; 32673 MW; FOBCDBC37DEDF3C5 CRC64;
PROBABLE PRECORRIN-6X REDUCTASE (EC 1.3.1.54).
                                        Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000873; AAB85498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 24.5%
                                                                                                                    SEQUENCE FROM N.A.
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                                                                                Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase;
SEQUENCE 302 A
                       COBK OR MIH1002
                                                                                                                                           STRAIN-DELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMH OR MIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 3:125-131(1994).
-!- FUNCTION: THIS GLYCOPROTEIN, PRODUCED BY THE SERTOLI CELLS OF THE TESTIS, CAUSES REGRESSION OF THE MUELLERIAN DUCT. IT ALSO IS ABLE TO INHIBIT THE GROWTH OF TUMORS DERIVED FROM TISSUES OF MUELLERIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHERWISE NORMAL MALES.
-!- MISCELLANDOUS: ALTHOUGH IT DOES NOT COMPETE WITH EGF FOR RECEPTOR BINDING SITES, MIS CAN INHIBIT THE AUTOPHOSPHORYLATION OF THE EGF RECEPTOR IN VITRO.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                              Damerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Ouan G.,
Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
Cate R.L., Mattaliano R.J., Hession C., Tizard R., Farber N.M., Cheung A., Ninfa E.G., Frey A.Z., Gash D.J., Chow E.P., Fisher R.A., Bettonis J.M., Torres G., Wallner B.P., Ramachandran K.L., Ragin R.C., Manganaro T.F., McLaughlin D.T., Donahoe P.K., Isolation of the bovine and human genes for Mullerlan inhibiting substance and expression of the human gene in animal cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
DISEASE: DEFECTS IN AMH ARE THE CAUSE OF PERSISTENT MUELLERIAN
DUCT SYNDROME (PMDS); A FORM OF MALE PSEUDOHERMAPHRODITISM
CHARACTERIZED BY A FAILURE OF MUELLERIAN DUCT REGRESSION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular genetics of the persistent mullerian duct syndrome: a study of 19 families.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Variants of the anti-Mullerian hormone gene in a compound heterozygote with the persistent Mullerian duct syndrome and his
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS PMDS G-12; P-70; V-101; W-123; C-167; C-194 AND A-477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carre-Eusebe D., Imbeaud S., Harbison M., New M.I., Josso N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imbeaud S., Carre-Eusebe D., Rey R., Belville C., Josso N. Picard J.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
MUELERIAN INHIBITING FACTOR.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA; 1.
PRAM: PF00019; TGF-DETA; 1.
Growth factor: Glycoprotein; Gonadal differentiation; Speudohermaphroditism; Disease mutation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Genet. 90:389-394(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K03474; AAA98805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC005263; AAC25614.1;
PIR; A01397; WFHUM.
                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT ARG-325.
MEDLINE; 93131268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94214429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUCT ORIGIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
26
462
488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQL--KLTDGS--AHRFEVPIAKFQEL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    884 QGKDTPNLT----RSDVLGKAFAVTQSLLGDGLIQAGHDVSDGGLLVCVLEMAIGGLSGL 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 ---VGALHGKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLK---- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PDAFQEELQELGIPQDLIGDLASLAFGSQRPLL-------DSVAQ---Q 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 SHSGIATSIGTQPLKGLLDPAAMARMCVAEALSNL---VFVKISELADVKCSGNWMWAAK 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Wickenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Sprigss T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
        L-GLUTAMINE + H(2)O = ADP + ORTHOPHOSPHATE + 5'-PHOSPHORIBOSYL-FORMILGLYCLINAMIDINE + L-GLUTAMATE.

PATHMAY: FOURTH STEP IN DE NOVO PURINE BIOSYNTHESIS.

SIMILARITY: TO E.COLI ENZYME (PURL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 SHSGRVSFLGSQP----SPBVTA---VAQLLKDLDRSTFRKLLKLV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         834 STYAPCPDV-----RLKVTPDLKGPGA----GSKTSLLWINLENSARLGGSALAQAYAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
ACETYL-COENZYME A CARBOXYLASE CARBOXYL FRANSFERASE SUBUNIT ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         FLYBASE; FBGN000052; ade2.
PFAM; PF00586; AIRS; 1.
PUTING blosynthesis; Ligase.
SEQUENCE 1354 AA; 148195 MW; 30AF726DFF0353A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.3%; Score 81.5; I
23.5%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    940 RVDLSEPLAKLKNFDKSVEK 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYSVALVLKEMAELEKKCER 220
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00683; AAC46468.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
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MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCA OR HI0406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCA_HAEIN
P43872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 6.4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ACCA_HAEIN
ACCA_HAEIN
ACCA_HAEIN
DT 01-NOV
DT 01-NOV
DE 01-NOV
DE 01-NOV
DE 02-NOV
DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 LOALLEGDDHRCFTRMTPALLLLPRSEPAPLPAHGQLDTVPFPPPRPSAELEESPPSADP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 ---THTLLQQALRLPPA-----SLKPDAFQEELQELGIPQDLI--GDLASL--AFGSQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 FLETLTRIVRALRVPPARASAPRLALDPDAL-----AGFPQGLVNLSDPAALERLLDGE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 PSPEVTAVAQLL---KDLDRSTFRKLLKLVV----GALHGKDCREAVEQLGASANLSEER 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PHOSPHORIBOSTIFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM
SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT)
(ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 RPLL-------DSVAQQGSSLPHVSYFRWRVDVAI-STSAQSRSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 EPLLLLLRPTAATTGDPAPLHDPTSAPWATALARRVAAELQAAAAELRSL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                          INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_007492.
A -> V (IN REF. 2).
3EFC2EE4FECC364C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FIId-VAR_007489.
R -> C (IN PMDS).
/FIId=VAR_007490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                          /FTIG=VAR_007485
G -> V (IN PMDS)
/FTIG=VAR_007486
                                                                                                              V -> G (IN PMDS)
/FTId=VAR_007483
                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_007488
                                                                                                                                                                                                       FTIG=VAR 007484
                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_007487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG-VAR 007491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V -> A (IN PMDS)
                                                                                                                                                                                                                                                                                                                                                R -> W (IN PMDS)
                                                                                                                                                                                                                                                                                                                                                                                                      (IN PMDS)
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pred. No. 20;
17; Mismatches
                                                           POTENTIAL.
                                                                                      POTENTIAL.
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Best Local Similarity 23.5%;
Matches 54; Conservative 1
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59192
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560 AA;
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MEDLINE; 94095139.
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  192
525
64
329
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P35421;
DISULFID
DISULFID
CARBOHYD
CARBOHYD
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13;

Gaps

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Science 269:496-512(1995).

-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A CARBOXYLASE COMPLEX: FIRST, BIOTIN CARBOXYLASE CATALYZES THE CARBOXYLATION OF THE CARRIET PROTEIN AND THEN THE TRANSCARBOXYLASE TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SIMILARITY).

-I- CATALYTICA ACTIVITY: CARBOXYL CARRIER PROTEIN + MALONYL-COA.

ACETYL-COA - BIOTIN CARBOXYL CARRIER PROTEIN + MALONYL-COA.

-I- PATHWAY: FIRST STEP IN LONG-CHAIN FATTY ACID SYNTHESIS.

-I- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).

-I- SIMILARITY: TO THE C-TERMINUS OF MANMALIAN PROPIONYL-COA
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 PGAYPGIGA----EER-----GQAEAIARNLR-------EMAQLTVPVICTV 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 HQKGRSVKEKVQRNFGMPAPE-------GYRKALRLMEMAERFKLPIITFIDT 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 HHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALHGK-----DC 64
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"Nucleotide sequence of a radiation leukemia virus genome.";
virology 158:88-102(1987).
-i- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO XIELD MATURE PROTEINS.
-i- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-POL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.2%; Score 80.5; DB 1; Length 315; Best Local Similarity 25.8%; Pred. No. 13; Matches 61; Conservative 28; Mismatches 74; Indels 7:
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01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fatty acid biosynthesis; Ligase.
SEQUENCE 315 AA; 35126 MW; E3B0B498A2686B23 CRC64;
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P11227;
       Science
-1- FUNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Gaps
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BUDDILINE; 9126087.
HOLZbaur El.F., Hammarback J.A., Paschal B.M., Kravit N.G.,
Pfister K.K., Vallee R.B.;
Homology of a 150K cytoplasmic dynein-associated polypeptide with
the Drosophila gene Glued.";
Nature 331:579-580(1991).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE)
(DP-150) (DAP-150) (P150-GLUED).
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Pfister K.K., Vallee R.B.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
fw; 9549253FCEEB5306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM: PF00078; rvt; 1.
PFAM: PF00552: integrase: 1.
PFAM: PF00552: rve; 1.
PFAM: PF00655: rve; 1.
Agratyl protease: Endonuglease: Polyprotein.
CHAIN 1 103 PROTEASE.
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 67;
30; Mismatches
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PROSITE; PSCOL141; ASP_PROTEASE;
PRAM; PFO0075; rnaseH; 1.
PFAM; PFO0077; rvp; 1.
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Best Local Similarity 24.2%
Matches 54; Conservative
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SEQUENCE
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Wozniak R.W.,
"POM152 is an
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CARBOHYD
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB outstation the Lucopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              11;
FUNCTION: REQUIRED FOR THE CYTOPLASMIC DYNEIN-DRIVEN RETROGRADE MOVEMENT OF VESICLES AND ORGANELLES ALONG MICROTUBULES. DYNEIN-DYNACTIN INTERACTION IS A KEY COMPONENT OF THE MECHANISM OF AXONAL TRANSPORT OF VESICLES AND ORGANELLES.
SUBBUNIT: LARGE MACROMOLECULAR COMPLEX OF AT LEAST 10 COMPONENTS.
P150(GLUED) BINDS DIRECTLY TO MICROTUBULES AND TO CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 D------LIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRSLQPSVLMQLKLTD--GSAHRFEVPIAKFQELRYSVALVLKEMAE------LEKKCE 219
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  20 GRV-SFLGSQPSPEVTAVAQLLKDLDR--STFRKLLKLVVGALHGKDCREAVEQLGASAN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 VSDTLLDCRKHLTWVVAVLQEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POM152 OR YMR129W OR YM9553.05.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                              -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: CONTAINS 1 CAP-GLY DOMAIN.
-!- SIMILARITY: STRONG, TO OTHER SPECIES DYNACTIN 150 KD SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      882 SSPYECLROSCSILISTMNKLATAMQEGEYD--AERPPSKPPPVE--PW------
                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                          Motor protein; Microtubules; Dynein; Coiled coil; Cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
WW. C9348CF129F4FF5C CRC64;
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01-OCT-1996 (Rel. 34, Last annotation update)
NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POMI52 (P150).
                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1337 AA
                                                                                                                                                                                                                                                                                                                                                                                                           34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 80.5; 23.7%; Pred. No. 73;
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                                                                                                                                                                                                                                                                                                  SER-RICH.
                                                                                                                                                                                                                                                                                       CAP-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                      PIR; S16129; S16129.
PROSITE; PS00845; CAP_GLY; 1.
PFAM; PF01302; CAP_GLY; 1.
                                                                                                                                                                                                                           EMBL; X62160; CAA44091.1; -.
                                                                                                                                                                                                                                                                                                                                                  141929
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 23.7 tes 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                               513
1048
1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P152_YEAST
P39685;
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Matches
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                                                                                                                                                                         Walsh S.V.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGLGNVVDFTSLPEELKKRYDLSYNFNVHEVPRAALEERFDPKSPTKRSIAIVFEEI 542
Blobel G., Rout M.P.;
integral protein of the pore membrane domain of the
envelope ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ASLAFGSQRPL---LDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 NDLKWGRNQPVNINLDSSITQDGK-----FAYKID-----KIT
                                                                                                                                                                  Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF THE NUCLEAR PORE COMPLEX WHICH MAY PRO THE NECESSARY ASYMMETRY REQUIRED FOR ANCHORING STRUCTURES SUC CYTOPLASMIC FILAMENTS AND THE NUCLEOPLASMIC CAGE.
-!- SUBUNIT: INTERACTS WITH NUP170 AND/OR NUP188.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. NUCLEAR PORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CISTERNAL SIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A024A42069193898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Glycoprotein. RE SIDE (POTENTIAL).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                      -! - PTM: THE N-TERMINUS IS BLOCKED.
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(Rel. 34, Last seq:
(Rel. 35, Last anno
                                            ust nuclear envelope.";
Cell Biol. 125:31-42(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z31592; CAA83469.1; -. EMBL; Z48622; CAA88554.1; -.
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FILOPODIN (TALIN HOMOLOG)
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                                                                                                                        SEQUENCE FROM N.A. STRAIN-S288C / AB972;
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SGD; L0001464; POM1
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P54633;
01-0CT-1996
01-0CT-1996
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ID RB6K_MOUSE
AC P97329;
DT 15-FEB-2000
DT 15-FEB-2000
DT 15-FEB-2000
DE RABKINESIN-6
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MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                       RADIXIN, AND TALIN.
SIMILARITY: IN THE C-TERMINUS TO YEAST SLA2 AND C.ELEGANS 2K370.3.
PARTIAL, TO YEAST RODI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1483 LAHATSSLARAVKSVTSKEPGAKAMISQSLKDLESAINNLLITSSVPASERGIGIADFNK 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1543 LMSTCRSVSTASSQLIISA---SSCSQKPKDIELSSILSEN--AVLMINS---LKDIIKV 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
                                                                    Kreitmeier M., Gerisch G., Helzer C., Mueller-Taubenberger A.; "A talin homologue of Dictyostellum rapidly assembles at the leading edge of cells in response to chemoattractant."; "J. Cell Biol. 129:179-188(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                               -!- FUNCTION: ACTIN-BINDING PROTEIN THAT MAY BE INVOLVED IN THE COMPROL OF CELL MOTILITY AND CHEMOTAXIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC; RAPIDLY ASSEMBLES AT THE LEADING EDGE OF CELLS IN RESPONSE TO CHEMOATRACTANT.
-!- SIMILARITY: CONTAINS A DOMAIN FOUND IN BAND 4.1, EZRIN, MOESIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---STFRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.2%; Score 80.5; DB 1; Length 2491; Best Local Similarity 23.3%; Pred. No. 1.7e+02; Matches 52; Conservative 31; Mismatches 77; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 35, Last annotation update)
1NOSIRE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
(IU-NUCLEOSIDE HYDROLASE) (PURINE NUCLEOSIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268811 MW; B24FF0224F2A419B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAND 4.1-LIKE DOMÁIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structural protein; Cytoskeleton; Actin-binding, DOMAIN 134 294 BAND 4.1-LIKE DOMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LHHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDR---
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 Eukaryota; Dictyostellida; Dictyostellum.
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                                                                                                                                                                                                                                                                                                                                                                                          DICTYDB; DD01121; TALA.
PROSITE; PS00660; BAND_41_1; 1.
PROSITE; PS00661; BAND_41_2; 1.
PROSITE; PS50077; BAND_41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U14576; AAC46586.1; -.
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PFAM; PF01608; I_LWEQ; 1
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                             SEQUENCE FROM N.A.
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Q27546;
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1D 1UNH_CERTRA
AC 027546
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Degano M., Gopaul D.N., Scapin G., Schramm V.L., Sacchettini J.C.;

Three-dimensional structure of the inosine-uridine nucleoside N-
Tribohydrolase from Crithidia fasciculata...;

Biochemistry 35:5971-5981(1996).

-I- FUNCTION: CATALYZES THE HYDROLYSIS OF ALL OF THE COMMONLY

OCCURRING PURINE AND PYRIMIDINE NUCLEOSIDES INTO RIBOSE AND THE
ASSOCIATED BASE, BUT HAS A PREFERENCE FOR INOSINE AND URIDINE AS SUBSTRATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 ----DRVKEVVLMGGGYHEGNATSVAEFNIIIDPEAAHIVFNESWQVTMVGLDLTHQAL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Gaps
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Gopaul D.N., Meyer S.L., Degano M., Sacchettini J.C., Schrämm V.L., Inosine-uridine nucleoside hydrolase from Crithidia fasciculata. Genetic characterization, crystallization, and identification of histidine 241 as a catalytic site residue.";
Biochemistry 35:5963-5970(1996).
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15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
RABKINESIN-6 (RAB6-INTERACTING KINESIN-LIKE PROTEIN) (KINESIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 VGNQTLAKVTRNAQLVADIAGITGVPIAAGCDKPLVRKI--MTAGHIHGESGMGTVAYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: HOMOTETRAMER.
-!- MASS SPECTROMETRY: MW-24194; MW_ERR-4; METHOD=ELECTROSPRAY.
-!- SIMILARITY: BELONGS TO THE IUNH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: A N-D-RIBOSYLPURINE + H(2)0 - A PURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 EFKNKVDERHAVNLIIDLVMSHEPKTITLVPTGGLTNIAMAARLEPRIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H->A: LOSS OF ACTIVITY.
21B51B3878A73FA1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80; DB 1;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.2%; Score 80; 20.5%; Pred. No.
                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
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PFAM; PF01156; IU_nuc_hydro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U43371; AAC47119.1; -. PDB; 1MAS; 17-AUG-96. PDB; 2MAS; 12-AUG-97.
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240
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314 AA;
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hes 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                             517 PSLHSFIKKHSPQVGPGLEKEDKADSDLEDSPEDEADVSVYGKEELLQVVEAMKALLLKE 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 FRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 QSRSLQPSVLMQLKL----TDGSAHRFEVPI-------AKFQELRYSVALVLK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AFOEELQELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 80; DB 1; Length 887;
22.7%; Pred. No. 51;
tive 35; Mismatches 105; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 PYLHHPADSHSGRV-----SFLGSQP-----SPEVTAVAQLLKDLDRST 47
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y09632; CAA70845.1; -.
MGD: MGI:1201682; RABEKIFI.
PRINTS; PR00380; KINESINHEAVY.
PROSTIE; PS00411; KINESIN_MOTOR_DOMAIN1; FALSE_NEG.
PROSTIE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
PRAM: PF0A25; Kinesin; 1.
MOTOR protein; Microtubules; ATP-binding; Coiled coil; Golgi stack;
Protein transport.
                                                                                                                   Echard A., Jollivet F., Martinez O., Lacapere J.-J., Rousselet A.,
                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
7143CCB261A4EA15 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99876 MW;
                                                                         SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-TESTIS;
MEDLINE; 98101856.
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Best Local Similarity 22.78
Matches 58; Conservative
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ELQKLGQSLQSAERAC 760
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Search completed: May 15, 2000, 05:34:20 Job time: 12490 sec

Perfect score:

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Total number

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Searched:

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024061 salmonella
024185 drosophila
94930 moraxella c
066007 moraxella c
0951p4 mus musculu
09x1p4 mus musculu
09x1p4 mus musculu
073505 porcine end
022941 arabidopsis
09y2a5 homo sapien
02297 caenorhabdi
015028 homo sapien
099015 prototheca
092277 mus musculu
055160 homo sapien
099015 prototheca
09217 mus musculu
099015 homo sapien
099014 homo sapien
015312 homo sapien
015312 homo sapien
099014 homo sapien
099015 musculus norv
013023 homo sapien
099101 musculus norv
0683497 murine leuk
083497 murine sapien
     Q63829 mus musculu
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SEQUENCE FROM N.A.
TISSUB-PITUITARY TUMOR;
FU G., HUANG Q., SONG H., PENG J., ZHANG Q., MAO M., DAI M., MAO Y.,
ZHOU J., CHEN Z., CHEN J.;
"Human PIDOOS MRNA, complete cds.";
Submitted (JUL-1998) to the EMBL/Genbank/DDBJ databases.
EMBL; AF078857; AAD44489.1;
SEQUENCE 202 AA; 22966 MW; 51317189 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 SPEVTAVAQLLKDLDRSTFRKLLKLVVGALHGKD----CREAVEQLGASANLSEERLAVL 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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   Homo sapiens (Human).
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Q9Y6G5;
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Jesuorhabdi
P93792 triticum ae
043642 homo sapien
007732 saccharom
096936 drom
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097485 homo sapien
095017 chlamydia p
059152 agrobacteri
093117 caenorhabdi
063714 rattus norv
061493 drosophila
096373 plasmodium
096775 plasmodium
p93792 triticum ae
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076222 trypanoscra
054046 salmonella
054048 salmonella
09zvg0 arabidopsis
                                                                                                        May 15, 2000, 02:05:54 ; Search time 55.93 Seconds (without alignments) 277.684 Million cell updates/sec
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Q27512 caenorhabdi
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caenorhabdi
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                    225878 seqs, 69334122 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Match Length DB
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Maximum DB seq length: 1000000
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MEDLINE: 94150718.
MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., KERSHAW J., KIRSTEN T., HILLIER L., JIER M., JOHNSTON L.,
LIGHTNING J., LLOYD C., MEMDRRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STABEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN R., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
T. M. MEINSTOK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 -----PNDFADDQEDL---KNIIRYGELFKACHAINSTDFIQKSEDLKDEEKVALERIVE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 QQ-GSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQELRY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 LDRSTFRKLLKLVVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 PASLKPDAFQEELQELGIPQDLI--GDL--ASLAFGS--------QRPLLDSVAQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
-!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION IN US INVOLVED IN EXOCYTOSIS.
-!- SIMILARITY: TO OTHER PROTEINS OF THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                   Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annexin; Calcium/phospholipid-binding; Repeat.
SEQUENCE 676 AA; 74969 MW; 00E36C79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.4%; Score 104.5; DE
25.7%; Pred. No. 0.84;
ive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3027 AA
                        676 AA
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                         PRT;
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                                            J. NOV-1996 (TEMBLEEL 01, 01.NOV-1999 (TEMBLEEL 12, NEX-2 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00191; annexin; 4. PRINTS; PR00196; ANNEXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 229443; CAA82571.1;
HSSP; P79134; LAVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 25.7
nes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                        PRELIMINARY;
                                                                                                             Caenorhabditis elegans.
                                                                                                                                                            SEQUENCE FROM N.A
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Q9Y485;
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Matches
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RESULT
Q27512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1770 PFLRSMAYWILEDYSGALETLIKOPIRENDDOVLSASNPTVFNFYNYLR----THPLLL 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ASLKPDAFQ-EELQ 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LPPASLKPDAFQEELQELGIPQDLIGDLASLAFG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 SQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQ---LKL---TDGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 SQPSPEVTAVAQLLKDLDRSTFRK---LLKLVVG-----ALHGKDCREAVEQLGASAN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMPVPSAVPSANITLKEDSSTVSTASGILKTATGEVLVSCTALEGSSSTDALISLALGOI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 KLVVG-----ALHGKDCREAVEQLGASANLSEERL-----AVLLAGTHTLLQQAL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L., GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;
"Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AROUGES; AAD19159-11;
SEQUENCE 486 AA; 54694 MW; A5AOABBO CRC32;
                                                                                                                                                                                 homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 PYLHHPA----DSHSGRVSFLGSQP------SPEVTAVAQLLKDLDRSTFRKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 93; DB 2; Length 486;
21.9%; Pred. No. 4.9;
tive 35; Mismatches 100; Indels 58;
Homo sapiens.(Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.6%; Score 96; DB 4; Length 3027
Best Local Similarity 23.4%; Pred. No. 31;
Matches 65; Conservative 29; Mismatches 74; Indels
                                                                                           (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE C., SCHMIDT E.R.;
"Molecular analysis of the human DMXL1 gene, one of the P DmX from Drosophila melanquaster.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ005821;.CAA06718.1; -.
SENDEL; AJ005821;.CAA06718.1; -.
SENDENCE 3027 AA; 337828 MW; FDE10068 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            486 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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ses 54; Conserva
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Similarity
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01-MAY-1999
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RK 247
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Matches 5
                                                                                                                                                elegans
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Q63714;
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                                                                                                                                                                                                                                                                                                                                                                                                                          102 ASLKPDAFQEELQELGIPQDLIG---DLASLAFGS---QRPLLDSVAQQQGSSLPHVSYF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 Q-----HILLQQALRLPP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 GEKTYDFLRGNEPYKYFFGPEEHKLSCTLFRTRSGDNLGGTLHPRSVRFYYEQALKLYK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433
                                                                                                                                                                                                                                                                                                                                                                                                              ---ALHGKDCREAVE 69
   --WRVDVAI
                  EQTLPQOSSSKQSALSPRSLKPEISDSKQQQALQTPKDSAVRKHSEAPSPETQARASLSQ
                                                    SSSSQRSLPPQESAPERTLLEQQKASSFS-----PLSQFSAEKQKEALTTSKSHELYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                      STSAQSRSLQP-----SVLMQLKLTDGSAHRFEVPIAKFQELRYSVALVLKEMAELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 SGKKSEASIAFGQMLSAAPDHLGAQFGLANLAFDRGEFRKPRSPFSASSQQATNP--SSF
                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 584;
                                                                                                                                                                                                                                                                                    MATTHYSSE A.G., WHITE S., LIGHTFOOT R.,
"Genes required for cellulose synthesis in Agrobacterium
tumefaciens.";
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BURTON J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         16;
ELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFR-
                                                                                                                                                                                                                                                                                                                J. Bacteriol. 177:1069-1075(1995).
EMBL: L38609; AAC41431.1; -. SEQUENCE 584 AA; 65787 MW; 24782CA3 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.2%; Score 91; DB
Best Local Similarity 25.0%; Pred. No. 9.2;
Matches 53; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 AA
                                                                                                                                                                                                                                                                                                                                                                                                            22 VSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 RWRVDVAI-STSAQSRSLQPSVLMQLKLTDGS 186
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                                                                                                                                                     PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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01-FEB-1997 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 95164506.
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SEQUENCE FROM N.A.
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ERDQDRQ 240
                                                                              217 KCERKLQ 223
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Q59152;
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ESQUENCE FROM N.A.

MEDLINE, 94150718.

MISSON R., BAYNES C., BERKS M.,
MISSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MISSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RANDON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., KIRSHAW J., LAISTER L., JOHNSTON L.,
A JONES M., KIRSHAW J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RANDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MISG J., THOMAS K., VANDIN M., VAUGHAN K., WAPTERSTON R.,
MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOKI C., MISUMI Y., FUJIWARA T., SOHDA M., NISHIOKA M., IKEHARA Y.; Identification and characterization of rat 364 kDa Golgi-associated protein recognized by autoantibodies from a patient with rheumatoid arthritis."; Eunct. 22:565-577/1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell Struct. Funct. 22:565-577(1997).

-!- FUNCTION: MAY BE INVOLVED IN THE FORMATION AND/OR MAINTENANCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 HGKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPA--SLKPDAFQEELQELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSAQSRSLQPSVLMQLKLTDGSAHRFEVPI-----AKFQELRYSVALVLKENAELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 TSMREADLK--MLLELK-EMSSQQKDEIKALQKDVDTYQCQVENLQNSIEKLIRQNEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AAAPYLHHPADSHSGRVSFLGSQ-----PSPEVTAVAQLLKDLDRSTFRKLLKLVVGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 IPQDL-----IGDLASLA---FGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAIS
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01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
GIANTIN (GOLGI COMPLEX-ASSOCIATED PROTEIN OF 364 KD) (GCP364).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus
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Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 89.5; D. 23.6%; Pred. No. 8.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  THOMAS K.; Submitted (FEB-1995) to the EMBL/Ge EMBL; 281449; CAB03766.1; -. EMBL; 248241; CAB03766.1; JOINED. EMBL; 248241; CAA88286.1; -. EMBL; 281449; CAA88286.1; -. SEQUENCE 433 AA; 50444 MW; DB15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1277 LLLQEQINEQGLEI------QNLKAASHEAKAHTEQLKQELESSQLKIADLEHL 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AFGSQRPLLDSVAQQQGSSLPHVSYF-----RWRVDVAISTSAQS-----RSLQPSVLM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEEL-QELGIPQDLIGDLASL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LHHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALHGKDCREAVEQ 70
                    LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3187;
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19.2%; Pred. No. 20;
tive 54; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95; Indels
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PHISTRY M., SUNIO A., KRAMER H.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARO4926; AAC09301.1; -.
FLYBARE; FR90004376; Dvir/hook.
SEQUENCE 678 AA; 77198 MW; 9C59D23D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | : : | | : :| | 1383 QAKEHEERLKQVQVEICELKKQPKE----LEEESKAKQQQQRKLQ 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 QLKLTDGSAHRFEVPIAKFQELRYSVALVLKEMAELEKKCERKLQ 223
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                                                               coil; Transmembrane.
CYTOPLASMIC (POTENTIAL)
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MW; 3C55C2B9 CRC32;
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8.0%; Score 89; DB 11;
Best Local Similarity 21.8%; Pred. No. 1.3e+02;
Matches 49; Conservative 47; Mismatches 95;
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-!- SUBUNIT: DISULFIDE-LINKED HOWODIMER.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBI
BMEL; D25543; BAA65026.1; --
G0191 stack; Antigen; Coiled coil; Trans
                                                                                                              POTENTIAL.
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Best Local Similarity 19.29
Matches 53; Conservative
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                                                                                                                                                                                                                                                213 LQQELHKLOLEFARLEHNTIGDDGVSLGPIQAGSVRYNELRROLELVKEELLQSEGARED 272
                                                                                                                                                                                                                                                                                                                                       273 LKIKAQQQETDLLHM---QQRIDELMKSTAELTALKDEVDVLRESTDKLKVCEAQLETYK 329
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                             153 ELESSTRQTTEGGVVSSLSRNSLSGMLDGNAKALEERDAMAQKCFETEKKMLLLIDEKTN 212
                                                                                                                                                                                                   FQEELQEL-----GIPQDLIGD----LASLAFGSQR-------PLLDS----- 141
                                                                                                                                                                                                                                                                                                       ---VAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLM-----QLKLTDGSAHRFE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63; Gaps
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69
  --AVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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MEDINE: 97221599.
BOYD E.F., IJ J., OCHMAN H., SELANDER R.K.;
"Comparative genetics of the inv-spa invasion gene complex of Salmonella enterica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.7%; Score 85.5; DB 2; Length 336; Best Local Similarity 21.5%; Pred. No. 13; Matches 50; Conservative 40; Mismatches 80; Indels 6
                                                                                                       --GASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NELSON K., LI J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U43308; AAC45006.1; -
SEQUENCE 336 AA, 36507 \( \bar{W}W, \) D5C811AA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S3015;
MEDLINE; 97076912.
MEDLINE; 97076912.
MODECULAT GENETIC FELATIONSHIPS Of the SALMONELIAE.";
Appl. Environ. Microbiol. 62:804-808(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
     31 PEVTAVAQLLKDLDRSTFRKLLKLVVGALHGKDCRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                         330 KKLEEYNDLKKHVKMLEERSADYVQQNAQFEEDAKR 365
                                                                                                                                                                                                                                                                                                                                                                                                            192 VPIAKFQELRYSVALV-----LKEMAELEKKCER 220
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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GARDNER M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND L.,
KOONIN E.Y., STALLOM S., MASON T., YU K., FUJII C., PEDERSON J.,
SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,
SALZBERG S., ZHOU L., SUTTON G.G., CLAYTON R., WHITE O., SMITH H.O.,
FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.;
"Chromosome 2 sequence of the human malaria parasite Plasmodium":
                                        Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
RESA-H3 ANTIGEN.
                                                                                                                                                                                                                        EMBL: AE001424; AAC71972.1; -. SEQUENCE 1558 AA; 175658 MW; D49C2605 CRC32;
                                                                                                                                                                                                            Science 282:1126-1132(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                 SEQUENCE FROM N.A. MEDLINE; 99021743
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P93792
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                                                                                                                                                                                                                                                                                                                          MEDLINE: 94150718.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FITTON I.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAIVELE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFER I., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELG--IPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KLTDGSAHRFEVPIAKFQELRYSVALVLKEWA------------ELEKKCER
    -----PLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSR---SLQPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 674;
                      241 AQSKPVITIFPTLDGV-KGEDSSLIY-RFQRWGNDYSVNIQARQAGEFSLIPS
                                                                                                                                                                                                                                                                                    Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368.32-38(1994).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; Z80115; CAB02274.1; -.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  674 AA; 77728 MW; 159F7071 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1558 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
7.6%; Score 84.5; D
Best Local Similarity 21.2%; Pred. No. 39;
Matches 39; Conservative 30; Mismatches
                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1999 (TrEMBLrel. 12, C36B1, PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 KLQD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 SLQD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger
SEQUENCE
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                                                                                                   093343
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1245
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1109 ILEDYKELKTIETDILEEKKEIEKDHFEKFEEEAEBIKDLEADIIKEVSSLEVEEFKKLE 1168
                                                               Gaps
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                                                                                             27 SQPSPEVTAVAQILKDIDRSFFRKILKIVVGALHGRDCREAVEQLGASANLSEERLAVIL 86
                                                                                                                                                                                 87 AGTHTLLQQALRLPPASLKPDAFQEELQELG-IPQDLIGDLASL-----AFG
                                                                                                                      Triticum aestivum (Wheat).
Sukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
                                                                                                                                                                                                                                                                                                                                                              ------LIDGSAHRFEVP---IAKF----QELRYSVALVLKEMAELEKKCERKLQ
                                                           65;
                  Length 1558;
                                                                                                                                                                                                                                                                       133 SQRPLLDSVAQQQ---GSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 303;
15;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CHEYERNE;
ANDERSON O.D., CASSIDY B., DVORAK J.;
SUBMILTED (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 186028; AAB48477.1;
MENDEL, 14673; Triae, 2372.14673.
PRINTS; PRO0208; GLIADGLUTEN.
SEQUENCE 303 AA; 34197 MW; C53AD656 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
LOW-WOLECULAR-WEIGHT GLUTENIN STORAGE PROTEIN.
             ; Score 84.5; DB 5;
; Pred. No. 1.2e+02;
45; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.6%; Score 84; DB 1
27.3%; Pred. No. 15;
ative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
             7.6%;
Query Match
Best Local Similarity 21.68
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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12

Gaps

82;

Indels

86;

Length 790;

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2430 LGILEQALPLSEHFADSHQGLTAWLDDWEQQISRLSWPALRPDQITLQQDKNERLLQSIA 2489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 LQQALRLPPA--SLKPDAFQEELQELGIPQDLIGDLASLAFGSQRPLLDSVAQQQGSSLP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVS---YFRWRVDVAIS-TSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQ-'---- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HITKEKYDSLGLDILTDLTYVQSQNLIKNLLIVL------DIPLKTFLKIVPTIVI 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE; 99054752.

TRAKARD, D., VOLK T.;

"Kakapo, a novel cytoskeletal-associated protein is essential for the restricted localization of the neuregulin-like factor, vein, at the muscle-tendon junction site.";

T. Call Biol. 143:1259-1270(1998).

EMBL; Y09430; CAA70581.1; -.

HSSP; P07731; AA3: 1

NON_TER 1 1

SEQUENCE 4151 AA; 472264 MW; 5EEBBEC2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                           LHHPADSHSGRVSFLGSQPSPEVTAVAQL-----LKDLDRSTFRKLLKLVVGAL-- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------SEERLAVLLAGTHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517 LHFMQQQHSHKIKYLQKE--nALTKEQOFRLEKRRWHDILNLKEENFQKLKSELKGKLIL
Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6%; Score 84; DB 5; Length 4151;
19.1%; Pred. No. 4.7e+02;
ive 51; Mismatches 108; Indels 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSALGAAAPYLHHPADSHSGRVSFLG-----SQPS---PEVT----
                                                                      SEQUENCE FROM N.A. ALT-MORO M.; ALT-MOERBE J., SCHNEIDER C., MORO M.; SUDMITTEd (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                           DB 3;
52;
                                                                                                                                                                                                                    Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; 274287; CAA98819.1; -.
SEQUENCE 790 AA; 91739 MW; 6974F721 CRC32;
                                                                                                                                                                                                                                                                                                                                              ; Score 84; DB 3
; Pred. No. 52;
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELRYSVALVLKEMAELEKKCERKLQD 224
Fungi; Ascomycota; Hemi
setaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 21.4%;
Matches 57; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                         Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROOVIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 56; Conserv
                                                                                                                                                 [2]
SEQUENCE FROM N.A.
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096936
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  SORERERERES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHEN C.F., CHEN Y., DAI K., CHEN P.L., RILEY D.J., LEE W.H.; "A new member of the happO family of molecular chaperones interacts with the retinoblastoma protein during mitosis and after heat shock."; Mol. Cell. Biol. 16:4691-4699(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AFQEE----LQELGI----PQDLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSY----FR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 WRVDVAISTSAQSRSLQPSVLMQLKLTDGSAHRFEVPIAKFQELRYSVALVLKEMAELEK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 SPFSQQQQLVLPPQQQQLVQQQIPIVQPSVLQQLNPCKVFLQQQCSPVAMPQRLARSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 RKLLKLVVGALHGKDCREA-VEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPD 107
                                                                           SYFRWRVDVAISTSAQSRSL------QPSVLMQLKLTDGSAHRFEVPIAKFQELRYSV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPPQQSFSQQPPFSQQQQPL--PQQPSFSQQQPPFSQQQPPLSQQPPFSQQQPVLPQQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMITTER (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, ARO183354; AAC02679.1; -.
HSSP; PO2829; 1AH8.
PFAM: PFO0183; HSP90; 2.
PFAM: PFO0183; HSP90; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.6%; Score 84; DB 4; Length 649; Best Local Similarity 23.8%; Pred. No. 40; Matches 46; Conservative 39; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
CHROMOSOME IV READING FRAME ORF YDL219G.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649 AA; 74017 MW; CCAF787C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   790 AA
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                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                          :::| ::||
156 MWQQSSCHVMQQQCCQQLQ 174
                                                                                                                                                                             205 ALVLKEMAELEKKCERKLQ 223
                                                                                                                                                                                                                                                                                                                                                                                                     JN-1998 (TrEMBLrel. 06,
JN-1998 (TrEMBLrel. 06,
JV-1999 (TrEMBLrel. 12,
SHOCK PROTEIN 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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208 DCKEFSSEARVRD 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KC----ERKLQD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 96347537
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01-NOV-1999
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri May 12 10:32:27 2000; MasPar time 81.38 Seconds 190.847 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-223-796-4 (1-224) from US09223796.pep 1604 1 MSAVGAATPYLHHPGDSHSG.....ALVLKEMADLEKRCERRLQD 224 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

225878 segs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembil2
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 45.912; Variance 95.996; scale 0.478 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Autch Length DB ID	1.02e+00 1.35e+00 1.79e+00 2.36e+00	.02e+00	.35e+00	.02e+00	.71e-01	.81e-01	.36e-01	.27e-01	.45e-01	.27e-01	.27e-01	27e-01	64e-02	64e-02	69e-02	.42e-03	.42e-03	Pred. No.	
Score Match Length DB ID Description 125 7.8 195 11 Q63829 BNP-5 CF BMI-1 PRO 125 7.3 576 5 Q22M95 F5A8.3 PROTEIN. 113 7.0 1576 2 O69354 RECEPTOR-LIKE HIST 107 6.7 360 2 O33934 RECEPTOR-LIKE HIST 107 6.7 361 2 O54225 DTDP-4-KETO-6-DEOX 107 6.7 451 2 P72863 HYPOTHETICAL 49.7 108 6.5 902 4 O43632 SPINDLE COLE DOX 105 6.5 902 4 O43632 SPINDLE DOX BODY 103 6.4 40 2 COLET OF COLET O	4446	7.0	1.3	1.0	7.7	5.8	4.3	3.2	2.4	3.2	3.2	3.2	5.6	5.6	1.6	1.4	1.4	Pred	
Score Match Length DB Match Length DB 125 7.8 195 11 125 7.8 512 10 113 7.0 1576 2 107 6.7 463 2 107 6.7 463 2 107 6.7 463 2 108 6.5 6.6 902 4 108 6.5 711 11 103 6.4 4 764 4 102 6.4 1116 5 101 6.5 111 6 2 101 6.4 1116 5 101 6.4 116 6.4 1116 5 101 6.4 116 6.4 116 6.4 116 6.4 1116 5 101 6.4 116	LOID RECEPTOR- OLYMERASE III FSH, LH/CG REC MEMBRANE PROT	VANILLOID RECEPTOR-LIK	MCE-FAMILY PROTEIN.	PUTATIVE REGULATORY PR	LIPOXYGENASE-3.				PMGA, COMPLETE CDS.		DTDP-4-KETO-6-DEOXY-HE	ERYCII.			NEX-2 PROTEIN.	F5A8.3 PROTEIN.	BUP-5'OF BMI-1 PROVIRA	Description	
Score 125 125 113 113 113 107 107 107 108 108 103 103 103 103	Q9Y670 P73507 Q94979 Q44382	Q9Y5S1	053544	Q9ZBT5	Q9WV07	096777	043632	P73374	007346	P72863	054225	033934	005201	069354	027512	G92W95	063829	ΩI	
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Result NO. 11 12 12 12 12 12 12 12 12 12 12 12 12	103 102 101 100	103	102	.103	104	105	106	107	108	107	107	107	113	113	117	125	125	Score	
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2.36e+00	3.10e+00	2.36e+00	3.10e+00	2.36e+00	4.08e+00	4.08e+00	6.99e+00	5.34e+00	5.34e+00	5.34e+00	5.34e+00	5.34e+00	6.99e+00	5.34e+00	5.34e+00	5.34e+00	6.99e+00	9.13e+00	9.13e+00	9.13e+00	9.13e+00	9.13e+00	9.13e+00	9.13e+00
APOLIPOPROTEIN AIV.	SIMILARITY TO DIDP-GLU	GC-RICH SEQUENCE DNA-B	MYELOID/LYMPHOID LEUKE	RIBONUCLEOTIDE REDUCTA	REGULATORY COMPONENTS	POLYKETIDE SYNTHASE (F	MYX.	GALR-LACI HOMOLOG.	HOMOLOGUE OF REGULATOR	R12G8.2 PROTEIN.	MANNOSE-SENSITIVE HEMA	HEAT SHOCK PROTEIN 75.	HYPOTHETICAL 77.2 KD P	COME.	KIAA0644 PROTEIN.	KIAA0667 PROTEIN (FRAG	MYOSIN-RHOGAP PROTEIN,	P2 J HOMOLOG.	HYPOTHETICAL 37.1 KD P	BETAINE-ALDEHYDE DEHYD	RESTRICTION METHYLASE.	N-METHYL-D-ASPARTATE R	HYPOTHETICAL 169.2 KD	CDA PEPTIDE SYNTHETASE
093601	017556	095032	095836	P89462	P74288	053730	962912	084915	P94426	9VTX60	056676	043642	Q92A89	P73100	075139	075155	Q9Z1N3	037840	P71924	059808	P95799	093338	086560	092429
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366	631	753	1010	1142	368	1198	206	340	479	485	535	649	671	709	811	1111	2626	302	333	200	563	996	1557	2117
6.2	6.2	6.3	6.2	6.2	6.1	6.1	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	6.0	0.9	0.9	5.9	5.9	5.9	5.9	5.9	5.9	5.9
100	66	100	66	100	86	86	96	97	97	97	26	6	96	97	97	46	96	95	95	95	95	95	95	92
21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

PRELIMINARY; 96 (TrEMBLrel. 01, L2 99 (TrEMBLrel. 12, L6 BMI-1 PROVIRAL INSER! 1us, Mouse. 1us, Mouse. 93.165034. BAREL G., ADAMS J.M. RAGGORIA; SCIUTOGRA; RAGGORIA; ADAMS J.M. RAGGORIA; J.M. 195 AA; 22037 MW; 195 AA; 22037 MW; 195 AA; 22037 MW; 11 ABB25378.1; 195 AA; 22037 MW; 10 Inlarity 22.2%; Print ABB25378.1; 196 ABCOLVGDLASVYEGSORY 1: :: : : : : : : : : : 1: VLMOLKLSDGSAYRF-EVP-' PRELIMINARY; 99 (TEMBLREL 10, L0, L9 99 (TEMBLREL 10, L0, L9 99 (TEMBLREL 10, L0, L9 OTEIN.	RESULT 1 10 063829 AC 063829 DT 01-NOV-199 DT 01-NOV-199 DT 01-NOV-199 DE BUP-5 OF E BUR BUP. OC EURATYOCA OC OC EURATYOCA OC OC EURATYOCA OC OC EURATYOCA OC	SULT 1 PRELIMINARY; 063829 CAS829 CAS829 CAS829 CAS829 CAS829 CAS825 CAS	Mus musculus (Mouse). Eukaryota's Metazoa; Chor Eukheria; Metazoa; Chor Eutheria; Redentia; Sciul [1] SEQUENCE FROM N.A. MEDLINE; 93165034. HAUPT Y., BARRI G., ADAM "Nucleotide sequence of insertion locus."; Mol. Biol. Rep. 17:17-20 EMBL; S54914; ABR25378:11 MGD; MGI: 8218; Bup.	Query Sest Match		SULT 2 PRELIMINARY; 092W95; 01-MAY-1999 (TIEMBLIEL: 01-MAY-1999 (TIEMBLIEL: 01-MAY-1999 (TIEMBLIEL: F5A8.3 PROTEIN. F5A8.3 PROTEIN. F5A8.3 Arabidopsis thaliana (MC Arabido
PRT; 195 AA. reated) sst sequence update) sst annotation update) riow Locus. Craniata; Vertebrata; hi; Muridae; Murinae; in upstream gene in the ced. No. 1.42e-03; SOTAB4F1 CRC32; SOTAB4F1 CRC32; SOTAB4F1 CRC32; SOTAB4F1 CRC32; SOTAB4F1 CRC32; FEETLLGSIGRSLPHITDVSWR SSTAB4F1 CRC32; SOTAB4F1 CRC32; SOTAB4F1 CRC32; FEETLLGSIGRSLPHITDVSWR SSTAB4F1 CRC32; ASTANACQCQUALCHYADFRWR SOTABCLODIVG-KLKDASKSLE STATES SOTABCLODIVG-KLKDASKSLE FILDSVAQQCAWLPHYADFRWR FILDSVAQQCAWLPHYADFRWR FILDSVAQQCAWLPHYADFRWR STATES STATES SOTABCLODIVG-KLKDASKSLE FILDSVAQQCAWLPHYADFRWR FILDSVAQQCAWLPHY	PRELIMINARY; PRT; 195 AA. 6 (TIEMBLEE]. 01, Created) 96 (TIEMBLEE]. 01, Last sequence update) 99 (TIEMBLEE]. 12, Last annotation update) 99 (TIEMBLEE]. 12, Last annotation update) MAI-1 PROVIRAL INSERTION LOCUS. 10 Metazoa; Chordata; Craniata; Vertebrata; 10 Metazoa; Chordata; Craniata; Musinata; 10 Metazoa; Chordata; Craniata; Metazoa; Crasa; 11 Metazoa; Chordata; Metazoa; Crasa; 12 Metazoa; Chordata; Metazoa; Crasa; 13 Metazoa; Chordata; 14 Metazoa; Chordata; 15 Metazoa; Crasa; 16 Metazoa; Chordata; 17 Metazoa; Metazoa; Crasa; 18 Metazoa; Chordata; 19 Metazoa; Crasa; 19 Metazoa; Crasa; 10 Metazoa; Chordata; 10 Metazoa; Crasa; 11 Metazoa; Metazoa; Crasa; 12 Metazoa; Metazoa; Crasa; 13 Metazoa; Crasa; 14 Haliana; Menuse-aar Crasa; 15 Metazoa; Crasa; 16 Metazoa; Crasa; 17 Metazoa; Metazoa; Crasa; 18 Metazoa; Metazoa; Metazoa; 18 Metazoa; Metazoa; Metazoa; 19 Metazoa; Metazoa; Metazoa; 10 Metazoa; Metazoa; Metazoa; 10 Metazoa; Metazoa; Metazoa; 11 Metazoa; Metazoa; Metazoa; 12 Metazoa; Metazoa; Metazoa; 13 Metazoa; Metazoa; Metazoa; 14 Metazoa; Metazoa; Metazoa; 15 Metazoa; Metazoa; Metazoa; 16 Metazoa; Metazoa; 17 Metazoa; Metazoa; 18 Metazoa; Metazoa; 19 Metazoa; Metazoa; 10 Metazoa; 11 Metazoa; 11 Me		Mammalia; Mus. bmi-1 proviral	s 144 171		
	PRELIMINARY; (CITEMBLEGL 01, 15, 15, 15, 15, 16, (TrEMBLEGL 12, 15, 15, 16, 17, 17, 17, 17, 18, 18, 18, 18, 18, 18, 18, 18, 18, 18	PRT; 195 AA. reated) ast sequence update) ast annotation update)	Craniata; Vertebrata; hi; Muridae; Murinae; , , n upstream gene in the 827A84F1 CRC32;	core 125; DB 11; Leng red. No. 1.42e-03; 7; Mismatches 40; In NSLETLLGSIGRSLPHITDVSWR :::	SCNMEQLQDLVG-KLKDASKSLE :::::::::: : :: TAKFQELRYSVALVLKEMA-DLE	PRT; 512 AA. reated) ast sequence update) ast annotation update) ar cress).

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                                                                                                                                                                                                                                       346 DNVRDEVRQVCGQDGVPSVEQLSSL-TSLNKVINESLRLYPPATLLPRMAFEDIKLGDLI 404
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., MEDENSON G., BONESET J., COULSON A., BONESET J., COOPER J., COLLSON A., CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., JONES M., KERSHAW J., LAYELIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., LAISTER N., LATREILLE P., LIGHTHING J., LLOYD C., MEMBRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., STADEN R., SUNTH A., SONNHAMMER E., STADEN R., SULSTON J., WHITS J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.)
                                                                                                                                                                                                                                                      62 EDCRDGVQRLGVSANLPE-EQLGALLAGMHTLLQQALRL-PPTSLKPD-TFRD-QLGELC 117
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Secennentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: CALCIDM, PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS.
-1- SIMILARITY: TO OTHER PROTEINS OF THE ANNEXIN FAMILY.
                                                                                                                                                                                                                    5;
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                                                                                                                                                                                           Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 676;
                                                                                                                                                                                       / Match 7.8%; Score 125; DB 10; Length 51 Local Similarity 33.8%; Pred. No. 1.42e-03; Local 22; Conservative 20; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 117; DB 5; Length 676
Pred. No. 1.69e-02;
26; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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PFAM; PF00191; annexin; 4.
PRINTS; PR00196, ANNEXIN.
PRINTS; PR01194, Phospholipid-binding; Repeat.
SEQUENCE 676 AA; 74969 MW; 00E36C79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                    676 AA
                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                     ULT 3 Q27512 PRELIMINARY; Q27512; Q27512; Q1-NOV-1996 (TTEMBLREL. 01, CA 01-NOV-1999 (TTEMBLREL. 12, L4 01-NOV-1999 (TTEMBLREL. 12, L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.3%;
Best Local Similarity 22.5%;
Matches 7.16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 229443; CAA82571.1;
HSSP; P79134; 1AVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        405 IPKGL 409
                                                                                                                                                                                                                                                                                                                 118 IPQDL 122
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134 ORPLIDSVAQQQ-GAMLPHVADFRWRVDVAISTSALARSLQPSVLMQL-KLSDGSAYRFE 191
132 EKVALERIVEOKLAESAKNEKDIAWNVNIVVANSYVAKSLRPVINIQMPTVGGDTNFEFD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 MLGDSGVGKSR-LLE-AVSEHAAQHSKVTVLRAARFDQAPARPLGPFSSVFRDLAAH-LR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 LIGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARAI H., KOSONO S., TAGUCHI K., MAEDA M., FUJI F., CHUNG S., SONG KUDO T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOSONO S., MAEDA M., FUJI F., ARAI H., KUDO T.;
Three of the seven bphC genes of Rhodococcus erythropolis TA421,
isolated from a termile ecosystem, are located on an indigenous
plasmid associated with biphenyl degradation.",
EMBL, AB014348; BAA3451.1;
EMBL, D88015; BAA35609.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodococcus sp.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113; DB 2; Length 1576
Pred. No. 5.64e-02;
18; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Two sets of the biphenyl degradation genes on a linear Rhodococcus erythropolis TA421."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              or-Aug-1999 (TrEMBLrel. 11, Last sequence update) 01-Aug-1999 (TrEMBLrel. 11, Last annotation update) PRECEPTOR-LIKE HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-JUL-1997 (TrEMBLrel. 04, Last annotation update) RECEPTOR-LIKE HISTIDINE KINASE BPDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor, Kinase, Plasmid; Hypothetical protein. SEQUENCE 1576 AA; 171035 MW; 636B3907 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 THPSELQR-V-REELGELIVVVGDQVPELAGA-FGGQAP 406
                                                                                                                                                                                                                     PRT; 1576 AA.
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                                                                                                                                                                                                                                                                Created)
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LABBE D., GARNON J., LAU P.C.K.;
J. Bacteriol. 179:0-0(0).
                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07,
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Local Similarity 30.3%;
hes 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Rhodococcus erythropolis.
                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                : : | |:|
192 VPT-AKF-QEL 200
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                                                                                    192 IDSFAOFROOL
                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pTA421
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069354
069354;
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7;

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Query Match

SO B

Matches

셤 ò 엄 ò LT 6 033934 033934;

RESULT

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STRAIN-PCC6803;
MEDLLES 97061201.
KANEKO T. SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIMI N., HIROSAWA M., WURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAWADA M., YASUDA M.,
TABATA S.;
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EMBL; D90901; BAA16879.1; -.

Hypothetical protein.

SEQUENCE 451 AA; 49667 MW; EEC3F698 CRC32;
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STRAIN-NRRL2338;
SALMH-BEY K., DOUMITH M., MICHEL J.M., HAYDOCK S., CORTES J.,
LEADLAY P.F., RAYNAL M.C.;
SUDMITTER (JUL.197) to the EMBL/GenBank/DDBJ databases.
EMBL; X14332; CAA74711.1;
PFAM; PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                                                Score 107; DB 2; Length 361;
Pred. No. 3.27e-01;
36; Mismatches 54; Indels
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Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
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Last sequence update)
Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JAN-1999 (TEMBLrel. 09, Last annotation update)
HYPOTHELICAL 49-7 KD PROTEIN.
                                                                                                                                                                                                                                                                                       SFC27F6A CRC32;
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07,
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Best Local Similarity 25.2%;
Matches 33; Conservative
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STRAIN-NRRL 2338;
MEDLINE; 98015410.

SUBMERS R.G., DONADIO S., STAVER M.J., WENDT-PIENKOWSKI E.,
HUTCHINSON C.R., KATZ L.;
"Sequencing and mutagenesis of genes from the erythromycin
biosynthetic gene cluster of Saccharopolyspora erythraea that are
involved in L.mycarose and D-desosamine production.";
microbiology 143:0-07(0).

EMBL; U77454; ABB84066.1; -.

PFRAM; PF00067; ABB84066.1; -.

SEQUENCE 360 AA; 38420 MW; D5E834E6 CRC32;
                                                                                                                                                                                                         7:
                                                                                                                        Length 1576;
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                                                                                                                        Score 113; DB 2; Length 157
Pred. No. 5.64e-02;
18; Mismatches 44; Indels
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharopolyspora erythraea (Streptomyces erythraeus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O54225, PRELIMINARY; PRT; 361 AA. O54225, O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 06, Last sequence update) O1-MAY-1999 (TrEMBLrel. 10, Last annotation update) DTDP-4-KETO-6-DEOXY-HEXOSE 3,4-ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ul-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ERYCII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 THPSELQR-V-REELGELIVVVGDQVPELAGA-FGGQAP 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107; DB 2;
Pred. No. 3.27e-01;
                                               2E087C0A CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 AA
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    EMBL; U85412; AAB52543.1; -. SEQUENCE 1576 AA; 170944 MW;
                                                                                                                        7.0%;
Local Similarity 30.3%;
nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.7%;
Best Local Similarity 25.2%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ODLVGDLASVV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 EHVIGEGEEVV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharopolyspora.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE: 98334402.
MURPHY S.M., URBANI L., STEARNS T.;
The mammalian gamma-tubulin complex contains homologues of the yeast spindle pole body components spc97p and spc98p.";
J. Cell Biol. 141:663-674(1998).
EMBL: AF042379; AAC39728-1;
SEQUENCE 902 AA: 102533 MW; A4ED2937 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 PATDAKQGFLRNQLQALFQPTD--NKLAMKLFGSKKALMKERIRQKAAGHWVIHPCSSFR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heliothis virescens (Noctuid moth) (Owlet moth).
Bukaryota: Metazoa; Arthropoda; Tracheata; Haxapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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KRIEGER J., STROBEL J., VOGL A., HANKE W., BREER H.;
I'Identification of a cyclic nucleotide and voltage-activated ichannel from insect antennae.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ01264; CAA10110.1;
HSSP; P00514; IAPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SPINDLE POLE BODY PROTEIN SPC97 HOMOLOG.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIC NUCLEOTIDE AND VOLIAGE-ACTIVATED ION CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 LEALLELALRMS-TA-NTOPFKDDLKIDL-MPHDLITQLLRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.36e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 4
Pred. No. 4.36e-
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             678 AA.
                                                                                                               902 AA
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                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%;
ilarity 37.2%;
Conservative
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                                                                                                               PRELIMINARY;
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Best Local Similarity
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                                                         LT 11
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043632;
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O967777
DT 01-MAY-1
DT 01-MAY-1
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DE CYCLIC N
GN CNG.
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CC DECTORYO'
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MEDLINES, 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMIRA T.,
HOSOCHI T., MATSUNO A., MUBAKI A., NAKAZAKI N., NAKUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 QDDRLNLLLTEVKKDIENRGWSIYDEEKKQGKLR-HL-SLRIGQR-TGEMLLTLISAHKG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIGGFTXLPLEPLLQSPASL-GYRNKATYP-LSRSKTGQVQAGYYRKGSHRLVNINQCPV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::| ||: : :: : : | :| || | | |: ::::: | 78 PEEQLGALLAGMHILLQ-QALRIPPISLKPDTFROQLQELCIPQDLVGDLASVVFGSQRP 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 QDDRLNLLLTEVKKDIENRGWSIYDEEKKQGKLR-HL-SLRIGQR-TGEMLLTLISAHKG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 RVS-FLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRL-GVSA-NL 77
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 108; DB 2; Length 463;
Pred. No. 2.45e-01;
41; Mismatches 57; Indels 10;
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Pred. No. 3.27e-01;
41; Mismatches 57; Indels 10;
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stis sp. (strain PCC 6803).
Cyanobacteria; Chroccoccales; Synechocystis.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-ANN-1999 (TrEMBLrel. 09, Last annotation update)
HYPOTHELIOL 51.5 KD PROTEIN.
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                   SEQUENCE FROM N.A.
HIHARA Y., IKEUCHI M.;
PHALANDAYON. Res. 0:0-0(0).
SEQUENCE 463 AA; 51532 MW; 944134AF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18. 3:109-136(1996).
D90905; BAA17405.1; -.
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LLDSVAQQGAWLPHVADF 155
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Best Local Similarity 22.3%;
Matches 31; Conservative
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Best Local Similarity 22.3%;
Matches 31; Conservative
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TABATA S.;
    Synechocystis
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SEQUENCE 46
                                           Bacteria;
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MEDLINE; 97000351.
MEDLINE; 97000351.
RIDARHH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KINASHI H., HOPWOOD D.A.;
A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL034446; CAA22387.1;
EMBL; AL034446; CAA22387.1;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                               KINDIAN, JEDDY M., FUERSTENBERGER G., MARKS F., KRIEG P.;
"CDNA cloning, genomic structure, and chromosomal localization on the murine epidermis-type lipoxygenase.";
Genomics 58:158-164(1999).
EMBL: Y14655; CAB46101.1; -.
SEQUENCE 711 AA; 80578 MW; B9BFE292 CRC32;
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(1) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SETRAIN-NMRI; TISSUE-SKIN EPIDERMIS: SQUAMOUS CELL CARCINOMA; MEDLINE; 99296830.

MEDLINE; 99296830.

MEDLINE; 99296830.

MEDLINE; 99296830.
                                                                                                                                                                                                                                                                                                                         Score 104; DB 11; Length 711;
Pred. No. 7.71e-01;
14; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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SAUNDERS D.C., HARRIS D.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PUTATIVE REGULATORY PROTEIN.
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Best Local Similarity 35.0%;
Matches 14; Conservative
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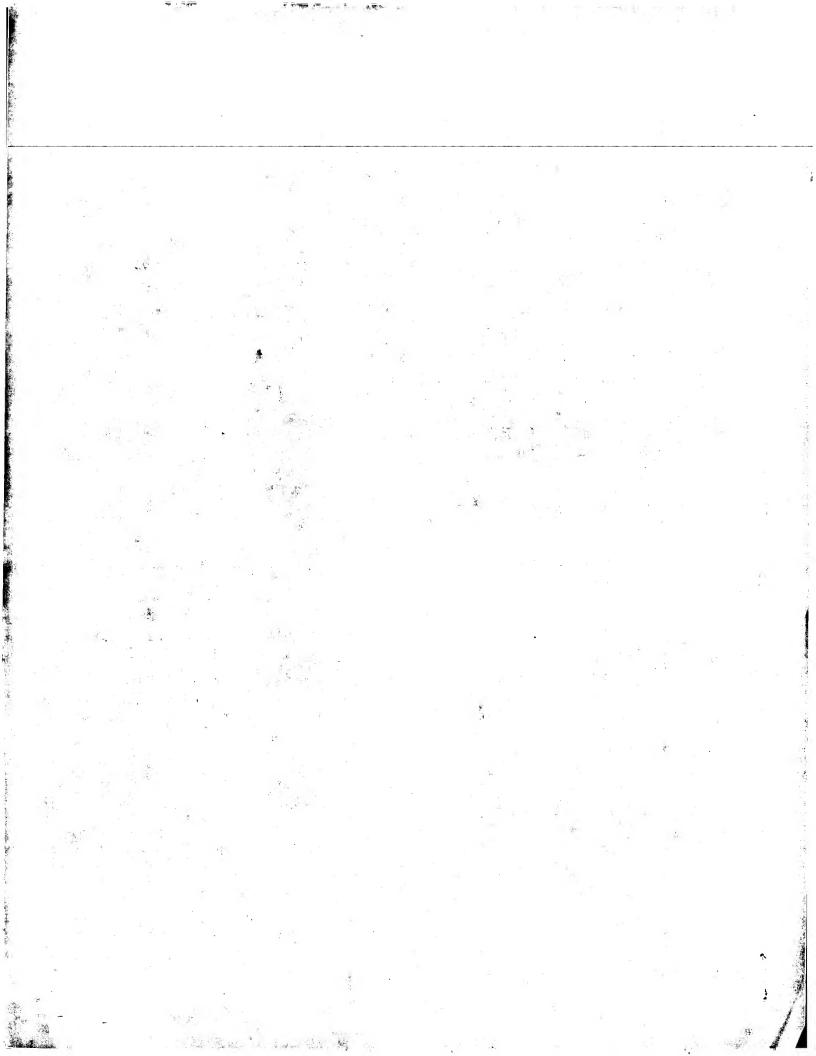
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                                                                               Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 GLNTLITRQANPKLP--ALQED-FRKAAVVANVYADAAGDLNTV-FDNLPTINKTIVDQ 237
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BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R.
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                                                                                                                                                                        BADCOCK K., CHURCHER C.M.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                          COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
 Created)
Last sequence update)
Last annotation update)
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EMBL; AL022022; CAA17736.1; -.
SEQUENCE 400 AA; 42418 MW; 8C21A90C CRC32;
(TremBLrel. 06,
(TremBLrel. 06,
(TremBLrel. 08,
                                                 MCE-FAMILY PROTEIN.
MTV023.06C.
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MEDLINE; 96181548.
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protein - protein database search, using Smith-Waterman algorithm Fri May 12 10:31:30 2000; MasPar time 34.81 Seconds 192.185 Million cell updates/sec Tabular output not generated. MPsrch_pp Run on:

>US-09-223-796-4 (1-224) from US09223796.pep 1604 Title: Description: Perfect Score: Sequence:

1 MSAVGAATPYLHHPGDSHSG......ALVLKEMADLEKRCERRLQD 224

PAM 150 Gap 11 Scoring table:

82229 seqs, 29864866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 47.835; Variance 94.148; scale 0.508 swiss-prot38 1:swissprot Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	5.73e-02	7.74e-02	7.74e-02	1.04e - 01	1.04e - 01	1.04e - 01	1.89e-01	4.54e-01	6.05e-01	8.05e-01	1.42e+00	1.42e+00	1.07e+00	1.07e+00	1.07e+00	1.87e+00	2.47e+00	2.47e+00	4.27e+00	5.60e+00	5.60e+00	5.60e+00	4.27e+00
Description	E1A-ASSOCIATED PROTEIN	NODULATION PROTEIN NOL	NODULATION PROTEIN NOL	PUTATIVE UROPORPHYRIN-	LIPH PROTEIN.	BASEPLATE ASSEMBLY PRO	LIPASE MODULATOR PRECU	PUTATIVE TRANSLATIONAL	GENOME POLYPROTEIN [CO	PUTATIVE SNRNP SM-LIKE	PHENYLALANYL-TRNA SYNT	FLAGELLAR M-RING PROTE	GC-RICH SEQUENCE DNA-B	HYPOTHETICAL ZINC AMIN	RIBONUCLEOSIDE-DIPHOSP	INVASIN PRECURSOR (OUT	GENERAL SECRETION PATH	TUMOR NECROSIS FACTOR	SHIKIMATE KINASE (EC 2	HYPOTHETICAL ABC TRANS	HYDROGENASE EXPRESSION	CYTOCHROME P450 2D15 (INSULIN-LIKE GROWTH FA
ID OI	P300_HUMAN	NOLW_RHIFR	NOLW_RHISN	HEMX_HAEIN	LIPH_PSEAE	VPJ_BPP2	LIMA_PSEAE	YAQ5_SCHPO	POLG_LMVE	RUXX_METTH	SYFA_SYNY3	FLIF_RHOSH	GCF_HUMAN	YIN7_YEAST	RIR1_HSV23	YADA_YERPS	GSPK_KLEPN	TRA1_HUMAN	AROK_SYNY3	YLIC_ECOLI	HOXV_AZOVI	CPDF_CANFA	ALS_RAT
DB	-	-	m	Н	Н	Н	Н	Н	Н	Ч	٦	П	П	1	Н	Н	Н	Н	Н	Н	Н	Н	Н
% Query Match Length	2414	234	234	230	282	302	340	2670	3255	81	331	570	784	946	1144	434	326	661	189	306	348	499	603
% Query Match	6.9	6.8	8.9	6.7	6.7	6.7	9.9	6.4	6.4	6.3	6.2	6.2	6.2	6.2	6.2	6.1	0.9	0.9	6.5	5.9	5.9	5.9	5.9
Score	110	109	109	108	108	108	106	103	102	101	66	66	100	100	100	98	97	97	95	94	94	94	92
Result No.	1	7	m	4	S	9	7	80	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23

5.60e+00 4.27e+00 7.32e+00	7.32e+00 7.32e+00 7.32e+00	7.32e+00 7.32e+00 7.32e+00	7.32e+00 7.32e+00	7.32e+00 1.24e+01 1.24e+01		1.24e+01 9.54e+00	3.54e+00 1.24e+01	1.24e+01 9.54e+00
PHOS IVAT KD	HYPOTHETICAL 63.1 KD P LAMIN B2. INSULIN-LIKE GROWTH FA	HYPOTHETICAL ACETYLCHO MINOR TAIL PROTEIN GP2 PROTEIN KINASE C-LIKE	HYPOTHETICAL 98.0 KD P GALACTOSE-INHIBITABLE	GENOME POLYPROTEIN (CO DFRA PROTEIN. INTERLEUKIN-2 PRECURSO	HYPOTHETICAL PROTEIN M TRANSCRIPTION FACTOR L	HYPOTHETICAL 44.4 KD P FUSION GLYCOPROTEIN PR	IN (CONT	HYPOTHETICAL 84.5 KD P HYPOTHETICAL 254.3 KD
RIR1_HSV11 GCN1_YEAST YDBI_SCHPO	YM19_YEAST LAM2_CHICK ALS_MOUSE	YZN4_CAEEL VG26_BPMD2 PKL2_RAT	YFIQ_ECOLI GIL1_ENTHI	POLG_LMVU DFRA_MYXXA II.2 CEREL	Y010_MYCPN LBX1_MOUSE	YJGN_ECOLI VGLF_MUMPM	YAB3_SCHPU ENV_RSVP	YA79_SCHPO YS89_CAEEL
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1137 2672 336	260 600 603	692 836 842	1276	3255 131 162	212 280	30 20 20 20 20 20 20 20 20 20 20 20 20 20	909 903	753 2329
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24 25 26	288	32 32	33 8 4 1	36 36 37	8 6 8 8	4 4 0	4 4	44 45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-USDA 257;
MEDLINE; 94018604.
MEINHARDT L.W., KRISHNAN H.B., BALATTI P.A., PUEPPKE S.G.;
"Molecular cloning and characterization of a sym plasmid locus that regulates cultivar-specific nodulation of soybean by Rhizobium fredii USDA257.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 LLAGMHTLLQQALRLPPTSLKPDTFRDQL-QELC-IPQDL-VG-DLASVVFGSQRPLLDS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSPREFLDRLTDLYDLQWYYDGVVLYVSA-AKEAQTRMLV-LSSVHFSAFKLALDKLDIS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFAGIHTTLGATLPLPSTSYKYTVLDQDLSAALQEFGNNLKISVNISAEVKGRIRGRIPE 83
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                          Plasmid sym.
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: REGULATES CULTIVAR-SPECIFIC NODULATION OF SOYBEAN. SIMILARITY: SOME, TO THE PULD/OUTD/EXED/XPSD FAMILY.
BINDING REGION FOR ELA ADENOVIRUS.
POLY-GLN.
POLY-GLN.
WW. ED6169CC CRC32;
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8
                                                                                                                                      2137 QAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQ-MNMNHNTM-PSQFRDILR 2184
                                                                                                                                                         Length 2414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 234;
                                                                                                           13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Indels
                                                                           Score 110; DB 1;
Pred. No. 5.73e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 109; DB 1; 1
Local Similarity 27.0%; Pred. No. 7.74e-02;
les 34; Conservative 35; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 36 POTENTIAL.
234 AA; 25829 MW; 87C798A5 CRC32;
                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
NODULATION PROTEIN NOLW
                                                                                                                                                                                                                                    234 AA
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S35020; S35020.
Plasmid; Nodulation; Transmembrane.
1572 1818 BIND
2066 2069 POLY
2190 2195 POLY
2414 AA; 264143 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 9:17-29(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L12251; AAB17675.1; -.
                                                                           Match 6.9%;
Local Similarity 34.0%;
les 17; Conservative
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Rhizobium fredii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 DERYPV 147
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ELRYSV 204
                                                                                                                                                                                                                 LT 2
NOLW_RHIFR
P33212;
                               DOMAIN
SEQUENCE
                                                                            Query Match
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DOMAIN
DOMAIN
                                                                                             Best Loca
Matches
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234 AA.

PRT;

NOLW_RHISN STANDARD; P55712; 01-NOV-1997 (Rel. 35, Created)

RESULT

486

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MEDITIE: 9535050
MEDITIE: 9535050
MEDITIE: 9535050
MEDITIE: 9535050
FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
KERLAYAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A.K., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SFRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRWANN J.L., GEOGRAGEN N.S.M.,
VENTER J.C.,
VENTER J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 LFAGIHTTLGATLPLPSTSYKYTVLDQDLSAALQEFGNNLKISVNISAEVKGRIRGRIPE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOY-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PUTATIVE UROPORPHYRIN-III C-METHYLITRANSFERASE (EC 2.1.1.107) (UROGEN
                                                                                                                                                                                                                                                                                                                       MEDLINE; 97305956.
FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A.,
                                                                                                                                                                                                        group;
                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
œ
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                Plasmid sym pNGR234a.
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae
Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 109; DB 1; Length 234 Pred. No. 7.74e-02; 35; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 387:394-401(1997).
-!- SIMILARITY: SOME, TO THE PULD/OUTD/EXED/XPSD FAMILY.
-!- SIMILARITY: SOME, TO Y4XJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
392E7F48 CRC32;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NODULATION PROTEIN NOLW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nodulation; Plasmid; Transmembrane.
TRANSMEM 17 38 POTENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000107; AAB91943.1; -.
                                                                                                                                  Rhizobium sp. (strain NGR234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%;
Best Local Similarity 27.0%;
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                            FROM N.A.
97305956.
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ELRYSV 204
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P44773;
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CALENDAR R.;
 Pseudomonas.
 LT 6
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 7;
 79 EEQLGALLAGMHTLLQQALRLPPTSLR-PDTFRDQLQELCIPQDLVGDLASVVFG-SQRP 136
 76 ENQTGANLSSNNTNNNKRLTQLEQSLKTAQENIAQLEQLIVSK--TGEITSLQTQMKQVS 133
 134 QL-AIAQQPSDWLFSEADFL--LNNALRKLVLDNDVDTAVSL-LKLADETLVK--VNNSQ 187
 Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: 2 S-ADENOSYL-L-METHIONINE + UROPORPHYRIN III
- 2 S-ADENOSYL-L-HOMOCYSTEINE + SIROHTDROCHLORIN.
-!- PATHMAX: INVOLVED IN THE BIOSYNTHESIS OF SIROHEME AND COBALAMIN.
-!- PATHMAX: MODERATE SIMILARITY TO E.COLI HEMX.
 56; Indels 10; Gaps
 Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
 SEQUENCE FROM N.A.
STRAIN-AICC 15692 / PAO1;
MEDLINE; 92381478.
WOHLEARTH S., HOESCHE C., STRUNK C., WINKLER U.K.;
"MOLECULAR genetics of the extracellular lipase of Pseudomonas aeruginosa PAO1.";
"Whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}\,.\,"\,;
 Length 230;
 Porphyrin biosynthesis; Transferase; Methyltransferase.
SEQUENCE 230 AA; 25193 MW; 432868A7 CRC32;
 Score 108; DB 1; 1
Pred. No. 1.04e-01;
 01-APR-1993 (Rel. 25, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
 34; Mismatches
 282 AA.
 Gen. Microbiol. 138:1325-1335(1992).
 PRT;
 EMBL; U32742; AAC22261.1; -.
 EMBL; X63391; CAA44998.1; -.
 188 ANEIRSAINQDLKQLLSL 205
 197 FOELRYSVALVLKEMADL 214
 Query Match 6.7%;
Best Local Similarity 27.5%;
 38; Conservative
 REVISION TO 244-274.
STRAIN-ATCC 15692 / PAOl;
 STANDARD;
 Pseudomonas aeruginosa
 WOHLFARTH S.;
 LIPH PROTEIN
 Pseudomonas.
 LT 5
LIPH_PSEAE
Q01725;
 Submitted
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 135 LSVAGSVGAYQYH-GRSADGRVADISVTSPSPACVTISVLSRENNGVASEDLLAVVRNAL 193
 NILSSEN O.
 1 MSAVGAATPYLHHPGDSHSGRVSFLGAQLP-PEVAAMARLLGDLDRSTFRKLLKFVVSSL 59
 150 LSAEEKAAAIDRL--RASLPEDQQESVLPQLQSELQQQTAALQAAGAGPEAIRQMRQQL 206
 Gaps
 HAGGARD-LJUNGQUIST E., JACOBSEN E., RISHOVD S., SIX E.W., NILSSEN O SUNSHINE M.G., LINDQVIST B.H., KIM K.-J., BARREIRO V., KOONIN E.V.,
 Gaps
 STRAIN-TE3285;
MEDLINE; 92337414.
CHIRARA-CIOMI M., YOSHIKAWA K., OSHIMA-HIRAYAWA N., YAMAWOTO K.,
SOGABE Y., NAKATANI T., NISHIOKA T., ODA J.;
 Bacteriophage P2.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
 ä;
 3,
 "Bacterlophage P2: genes involved in baseplate assembly.";
Virology 213:109-121(1995).
-!- FUNCTION: LIES AT THE EDGE OF THE BASEPLATE.
 DB 1; Length 302;
 Length 282;
 6.7%; Score 108; DB 1; Length 302
11.8%; Pred. No. 1.04e-01;
tive 18; Mismatches 39; Indels
 Score 108; DB 1; Length 282
Pred. No. 1.04e-01;
22; Mismatches 16; Indels
 LIMA_PSEAE STANDARD; PRT; 340 AA. 004591; P95420; 01-OCT-1993 (Rel. 27, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).
 EMBL; AF063097; AAD03284.1; -.
SEQUENCE 302 AA; 32780 MW; CB8BBA88 CRC32;
PIR; S25769; S25769.
SEQUENCE 282 AA; 31816 MW; 3252D3E5 CRC32;
 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1999 (Rel. 39, Last annotation update)
BASEPLATE ASSEMBLY PROTEIN J (GPJ).
 302 AA
 194 NGEDVRPVADRVTVQSAAIVEYQINATL 221
 60 OGEDCRDGVORLGV-SANLPEEQLGALL 86
 PRT;
 Best Local Similarity 31.8%;
 6.7%;
Local Similarity 30.5%;
les 18; Conservative
 28; Conservative
 STANDARD;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 MEDLINE; 96036485
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JT 9
POLG_LMVE
P89876;
 Potyvirus.
 CHAIN
 PEAM;
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 'n
 6
 Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: PARTICIPATES IN LIPASE PRODUCTION. THE LIPASE GENE IS
WELL EXPRESSED ONLY IN THE PRESENCE OF THIS PROTIEN WHICH EXERTS
ITS EFFECT BOTH IN CIS AND IN TRANS. IT MAY IN SOME WAY
PARTICIPATE IN THE SECRETION OF THE LIPASE (BY SIMILARITY).
-1- SIMILARITY: HIGH, WITH OTHER MODULATORS OF THE PRODUCTION OF
LIPASES IN OTHER PSEUDOMONAS SPECIES.
 CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V., Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
 208 LSTEEKAAAIDRL--RASLPEDQQESVLPQLQSELQQQTAALQAAGAGPEAIRQMRQQL 264
 21; Mismatches 17; Indels 3; Gaps
 Gaps
 Purification, molecular cloning, and expression of lipase from
 ;
9
 DB 1; Length 2670;
 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
PUTATIVE TRANSLATIONAL ACTIVATOR C18G6.05C (GCN1 HOMOLOG).
 Length 340;
 30; Indels
 Translation regulation; Activator. 997333 MW; 5C214AA7 CRC32;
 Eukaryota, Fungi, Ascomycota, Archiascomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
 Pred. No. 4.54e-01;
25; Mismatches 30;
 Pred. No. 1.89e-01;
 POTENTIAL.
LIPASE MODULATOR.
571A5FAC CRC32;
 DB 1;
 PRT; 2670 AA.
 Schizosaccharomyces pombe (Fission yeast).
 Pseudomonas aeruginosa.";
Arch. Biochem. Biophys. 296:505-513(1992).
 Score 103;
 Score 106;
 297333 MW;
 EMBL; AB008452; BAA23129.1; -.
 340 AA; 37686 MW;
 6.6%;
larity 30.5%;
Conservative
 Lipid degradation; Signal.
 6.48;
 larity 26.5%;
Conservative
 EMBL; 268198; CAA92385.1;
 STANDARD;
 l protein;
2670 AA; 2
 Schizosaccharomyces.
 S24161; S24161
 Local Similarity
 Local Similarity
les 22; Conser
 SEQUENCE FROM N.A.
 REVISIONS.
STRAIN-TE3285;
 YAQ5_SCHPO
Q10105;
01-FEB-1996 (
 18;
 Hypothetical
 SHIBATA H.;
 STRAIN-972;
 SEQUENCE
 SEQUENCE
 Query Match
 Query Match
 SIGNAL
 CHAIN
 Matches
 59
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Matches
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1664 ALGSLIEKLGEKKFPTLIPELFNVLRSE-CSE-VDRQGAAQGLSEI-LAGLGLARLEDVL 1720
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
COMPONENT PROTEINASE (EC 34, 1.22.-) (HC-PRO); PROTEIN (P1); GEND PROTEIN
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NIA)
(EC 3.4.22.-) (49 KD PROTEINASE) (49 KD-PRO); NUCLEAR INCLUSION
PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
COAT PROTEIN (CP)).
 II
 polymerase;
Helicase;
 Lettuce mosaic virus (strain E) (LMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 SEQUENCE FROM N.A.
MEDLLIES, 97.39892.
REVERS F., YANG S.J., WALTER J., SOUCHE S., LOT H., LE GALL O.,
CANDRESSE T., DUNEZ J.;
 SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6. SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4. SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
 6 KD PROTEIN 1.
CYTOPLASMIC INCLUSION PROTEIN.
6 KD PROTEIN 2
GENOME-LINKED PROTEIN.
 Hydrolase; Transferase; Thiol protease; RNA-directed RNA Coat protein; Polyprotein; Covalent protein-RNA linkage; ATP-binding.
 N-TERMINAL PROTEIN.
HELPER COMPONENT PROTEINASE.
 3255 AA
 PROTEIN P3
 PF00270; DEAD; 1.
PF00680; RNA_dep_RNA_pol; 1.
 1721 PEILKNTSSPV-PH-IRESFISL 1741
 94 QQALRLPPTSLKPDTFRDQLQEL 116
 PFAM, PF00767, Poty_coat, 1.
PFAM, PF00851, Peptidase_c6, 1.
PFAM, PF00863, Peptidase_C4, 1.
PFAM, PF01577, Poty_P1; 1.
 EMBL; X97705; CAA66281.1; -.
 STANDARD;
 INDIVIDUAL PROTEINS.
 CHAIN
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Rhodobacter.
 STRAIN-WS8;
 FLIF_RHOSH
Q53151;
 Matches
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 7:
 STRAIN-DELTA H;

X MIDLINE; 98037514.

SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
ALDREDGE T., BASHIRAADEH R., BLAKELY D., COOK R., GILBERT K.,
ALDREDGE T., BASHIRAADEH R., BLAKELY D., COOK R., GILBERT K.,
ALDREDGE T., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
A SPADAFORA R., VICARE R., WANG Y., WIESENSONSKI J., GIBSON R.,
A JIWANI N., CARUSO A., BUSH D., SAFER H., PIETROVSKI S., CHURCH G.M.,
A MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
A DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
T. Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltah: functional analysis and comparative genomics.";
J. Bacteriol. 179:1135-7155(1997).

C. -- SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY.
 1156 WVGVQVQGVKWLAKSVHYMIPELTNILNVGTLL-LTLISLGV-RFRSLTGQFKEMKYKET 1213
 148 WLP-HVADFRWRV-DVALSTSALARSLQPSVLMQLKLSDGSAYRFEVPTAKFQELRXSVA 205
 .
.
 8 RVNVQRPLDALGNSLNSPVIIKLK-GD-REFR-GVLKS-F-DLH--MNLVLNDAEELEDG 60
 Gaps
 8; Gaps
 Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 .;
9
 Score 102; DB 1; Length 3255;
Pred. No. 6.05e-01;
14; Mismatches 32; Indels
 Score 101; DB 1; Length 81;
Pred. No. 8.05e-01;
16; Mismatches 19; Indels
PROTEIN A. PROTEIN B.
 COAT PROTEIN.
ATP (POTENTIAL).
MW; A5475B9E CRC32;
NUCLEAR INCLUSION
NUCLEAR INCLUSION
 RUXX_METTH STANDARD; PRT; 81 AA. 026745; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) PUTATIVE SNRNP SW-LIKE PROTEIN.
 Hypothetical protein.
SEQUENCE 81 AA; 9061 MW; 60D0F649 CRC32;
 Pred. No. 6.05e-
14; Mismatches
 EMBL; AE000845; AAB85154.1; -. PFAM; PF01423; Sm; 1.
7 2977 1
2978 3255 (
1410 1417
3255 AA; 367621 M
 Query Match 6.3%;
Best Local Similarity 34.8%;
Matches 23; Conservative
 / Match 6.4%;
Local Similarity 27.8%;
nes 20; Conservative
 1214 LA-RE-EELRKR 1223
 1 :| :| ||
206 LVLKEMADLEKR 217
 SEQUENCE FROM N.A.
 Methanobacterium
 217 RCERRL 222
 61 EVTRRL 66
 NP_BIND
SEQUENCE
 Query Match
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 4
ou-nov-1997 (Rel. 35, Created)
01-Nov-1997 (Rel. 35, Last sequence update)
01-Nov-1997 (Rel. 35, Last sequence update)
PHENIALIANIL-TRNA SYNTHETASE ALPHA CHAIN (EC 6.1.1.20) (PHENYLALANINE-TRNA LIGASE ALPHA CHAIN) (PHERS).
 HSSP; P27001; 1PYS.
PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
PROSITE; PS00139; AA_TRNA_LIGASE_II_2; 1.
PFAM; PF01409; tRNA-synt_2d; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SEQUENCE 331 AA; 37124 MW; FA9E88E6 CRC32;
 SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
 33 RVQYLGKKGELSLILKGMGKLSAE-ERPKFGAIANEVKEALQHDLESRKANLQNAAIEAQ 91
 Gaps
 MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 96127529.
MEDLINE; 97.
MED
 Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 .;
2
 GOODFELLOW I.G., WOOLLEY K.J., SOCKETT R.E.S.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE M RING MAY BE ACTIVELY INVOLVED IN ENERGY
TRANSDUCTION (BY SIMILARITY).
 Pred. No. 1.42e+00;
23; Mismatches 24; Indels
 Score 99; DB 1; Length 331;
 PYROPHOSPHATE + L-PHENYLALANYL-TRNA(PHE).
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
(BY SIMILARITY).
 Bacteria; Cyanobacteria; Chroococcales; Synechocystis
 01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
FLAGELLAR M-RING PROTEIN.
 570 AA.
 PRT;
 Synechocystis sp. (strain PCC 6803)
 EMBL; D64001; BAA10328.1; -.
 Query Match 6.2%;
Best Local Similarity 27.8%;
 20; Conservative
 STANDARD;
 92 LAAETLDVTMAG 103
 77 LPEEQLGALLAG 88
 SEQUENCE FROM N.A.
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 ij
 that represses transcription.";

Cell 59:815-825(1989).

-I-FUNCTION: FACTOR THAT REPRESSES TRANSCRIPTION. IT BINDS TO THE GC-RICH SEQUENCES (GCGGGCC) PRESENT IN THE EPIDERMAL GROWTH FACTOR RECEPTOR, BETA-ACTIN, AND CALCIUM-DEPENDENT PROTEASE PROMOTERS.

-I-SUBCELLULAR LOCATION: NUCLEAR.

-I-TISSUE SPECIFICITY: WIDELY EXPRESSED IN HUMAN TISSUES AND CELL
 Transcription regulation; Repressor; DNA-binding; Trans-acting factor; Nuclear protein.
 KAGEYAMA R., PASTAN I.;
"Molecular cloning and characterization of a human DNA binding factor
SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L, P.S, AND M) MOUNTED ON A CENTRAL ROD. THE M RING IS INTEGRAL TO THE INNER MEMBRANE OF THE CELL AND MAY BE CONNECTED TO THE FLAGELLAR ROD VIA THE S RING. THE S (SUPRAMEMBRANE RING) LIES JUST DISTAL TO THE M RING. THE L AND PERIORS LIE IN THE OUTER MEMBRANE AND THE PERIOR SPACE, RESPECTIVELY (BY SIMILARITY).
 Gaps
 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 100 PPTSLKPDTFRDQLQELCIPQ-DLVGDLASVVFGSQRPLLDSVAQQQGAW 148
 402 PPPPLLPEALKADLERLTRSAVGFDADRGDVVTITAQPFLDTVVPEASGW 451
 Score 99; DB 1; Length 570;
Pred. No. 1.42e+00;
 18; Mismatches 17; Indels
 Eutheria; Primates; Catarrhini; Hominidae; Homo
 Flagella; Membrane.
SEQUENCE 570 AA; 60675 MW; IF8BGCE2 CRC32;
 SIMILARITY).
SIMILARITY: BELONGS TO THE FLIF FAMILY.
 784 AA
 PRT;
 EMBL; X98692; CAA67251.1; -. PFAM; PF01514; YSCJ_F11F; 1.
 EMBL; M29204; AAA35598.1; -.
 / Match 6.2%;
Local Similarity 28.0%;
les 14; Conservative
 STANDARD;
 Homo sapiens (Human)
 33; A33633
T00320; -
 SEQUENCE FROM N.A.
 90075226
 MIM; 189901; -.
 LT 13
GCF_HUMAN
P16383;
 LINES
 Query Match
 TRANSFAC;
 (TCF-9).
 Matches
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 STRAINS-SRB(C, AB972;
STRAINS-SLB(C, AB972;
STRAINS-SLB(C, AB972;
STRAINS-SLB(C, AB972;
STRAINS-SLB(C, AB972;
BARCELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
CHURCHER C.M., CONNOR R., COPSET T., DEAR S., DEVLIN K., FRASER A.,
GENTLES S., HAMIYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
WALSH S.V., WHITEHEAD S.,
SUDMITTEHEAD S.,
SUDMITTEHEAD S.,
SAMILARITY: BELONGS TO PEPTIDASE FAMILY MI (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE PEPN SUBFAMILY.
 299 GMITIQLNHLL-IPPNALANETVREQAQQL-IVHELVHQWMGNYISFDS-WESL-WFNES 354
 Gaps
 Gaps
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
 ;
 SIMILARITY).
 SIMILARITY).
 330 ZINC (CATALYTIC) (BY SIMILARITY).
331 BY SIMILARITY.
334 ZINC (CATALYTIC) (BY SIMILARITY).
21NC (CATALYTIC) (BY SIMILARITY).
107722 MW; 568EAFB6 CRC32;
 8
 534
 Length 946;
 Length 784
 Score 100; DB 1; Length 946
Pred. No. 1.07e+00;
21; Mismatches 20; Indels
 21; Indels
 485 PDSYYEAFISLCIPK-LLNPLIRVQLIDWNPLKLESTGLKEMPWFKSVEEF
 Ol-FEB-1995 (Rel. 31, Last sequence update)
01-MOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL ZINC AMINOPEPTIDASE VILL137C (EC 3.4.11.-).
 Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
 ASP/GLU-RICH (ACIDIC).
LEUCINE-ZIPPER.
 ARG/LYS-RICH (BASIC).
POLY-LYS.
 Score 100; DB 1;
Pred. No. 1.07e+00;
 LEUCINE-ZIPPER.
FE96504B CRC32;
 12; Mismatches
 946 AA
 PIR; S48397; S48397.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PFAM; PF01433; Peptidase_M1; 1.
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
01-NOV-1995 (Rel. 32, Last ann
 Ξ.
Έ
 6.2%;
ilarity 31.4%;
Conservative
 EMBL; Z38059; CAA86141.1; -.
78
86
29
230
380
740
 Match 6.2%;
Local Similarity 31.0%;
 Conservative
 STANDARD;
 355 FATWLACHILE 365
 ::||: |: |
QGAWLP-HVAD 154
 Query Match
Best Local Similarity
 946 AA;
 Aminopeptidase
 16;
 22;
 PIR; S48397,
PROSITE; PS(
 YIN7_YEAST
P40462;
 ACT_SITE
METAL
 SEQUENCE
 SEQUENCE
 Query Match
 DOMAIN
 DOMAIN
DOMAIN
 DOMAIN
 METAL
 METAL
 Matches
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 SEQUENCE OF 981-1144 FROM N.A.
MEDLINE, 84139764.
GALLOWAY D.A., SWAIN M.A.;
"Organization of the left-hand end of the herpes simplex virus type 2
B91II N fragment.;
J. Virol. 49:724-730(1984).
 -:- PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY.
-:- SUBUNT: HETERODIER OF A LARGE AND A SMALL CHAIN.
-:- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE
LARGE CHAIN FAMILY.
 Gaps
 SEQUENCE FROM N.A.
MEDLINE; 86144055.
SWAIN M.A., GALLOWAY D.A.;
Herpes simplex virus specifies two subunits of ribonucleotide reductase encoded by 3'-coterminal transcripts.";
J. Virol. 57:802-808(1986).
 ;
9
 01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (EC 1.17.4.1)
(RIBONUCLEOTIDE REDUCTASE) (136 KD SUBUNIT).
HERPES SIMPLEX VITUS (LYPP 2 / Strain 333).
Viruses; deDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
 Match 6.2%; Score 100; DB 1; Length 1144; Local Similarity 29.7%; Pred. No. 1.07e+00; les 27; Conservative 24; Mismatches 34; Indels
 224 231 POLY-ASP,
1144 AA; 125093 MW; 53E7FDD0 CRC32;
 EMBL; M12700; AAA45806.1; -.
EMBL; X00048; CAA44929.1; -.
PIR; A05247; A05247.
PROSITE; PS00089; RIBORED_LARGE; 1.
PRAM; PF00317; ribonucleo_red; 1.
Oxidoreductase; DNA replication; Early protein.
DOMAIN 151 159 POLY-PRO.
 PRT; 1144 AA.
 SECUENCE OF 1036-1144 FROM N.A. MEDLINE; 84057718.
 (Rel. 10, Created)
 STANDARD;
 THIOREDOXIN
 01-MAR-1989
 01-0CT-1996
01-0CT-1996
LT 15
RIRL_HSV23
P09853;
 SEQUENCE
 Query Match
 Best Loca
Matches
 RESULT
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324 ELTPENAEAVARFLGDAVDREP-ALMLEYFCRCAREESKRVPPRTFGSAPRLTEDDFGLL 382 :| :| :| :| | :::| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| | ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ..

383 NYALAEMRRICLDLPPVP--PNAYTPYHLRE 411 :: : | | | | | : | : | : | : | 86 LAGMHTLLQQALRLPPTSLKPDTFRD-QLQE 115

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Search completed: Fri May 12 10:32:10 2000 Job time: 40 secs.



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N. Table

| *****                                   | (TM)                                   |
|-----------------------------------------|----------------------------------------|
| ********                                |                                        |
| *******                                 |                                        |
| *************************************** | (MZ)                                   |
| ********                                |                                        |
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| * * *                                   | ************************************** |

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protein - protein database search, using Smith-Waterman algorithm Fri May 12 10:34:10 2000; MasPar time 54.28 Seconds 194.680 Million cell updates/sec MPsrch\_pp Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-09-223-796-4 (1-224) from US09223796.pep 1604 1 MSAVGAATPYLHHPGDSHSG.....ALVLKEMADLEKRCERRLQD 224

PAM 150 Gap 11 Scoring table:

142080 segs, 47172406 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Mean 46.697; Variance 102.828; scale 0.454

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|               |       | æ     |                       |    |        |                       |           |
|---------------|-------|-------|-----------------------|----|--------|-----------------------|-----------|
| Result<br>No. | Score | Query | Query<br>Match Length | DB | a      | Description           | Pred. No. |
| П             | 117   | 7.3   | 929                   | 7  | S41022 | hypothetical protein  | 3.05e-02  |
| 7             | 110   | 6.9   | 2414                  | 7  | A54277 | transcription adaptor | 2.18e-01  |
| m             | 109   | 9.9   | 234                   | ~  | S35020 | •                     | 2.87e-01  |
| 4             | 108   | 6.7   | 230                   | ~  | D64080 | uroporphyrin-III C-me | 3.78e-01  |
| 'n            | 108   | 6.7   | 283                   | ~  | S25769 | lipH protein - Pseudo | 3.78e-01  |
| 9             | 107   | 6.7   | 451                   | ~  | S74728 | ŭ                     | 4.96e-01  |
| 7             | 107   | 6.7   | 463                   | ~  | S77558 |                       | 4.96e-01  |
| 80            | 106   | 9.9   | 339                   | 7  | S24161 | ຜ                     | 6.50e-01  |
| σ             | 102   | 6.4   | 400                   | 7  | E70805 | probable mce4 protein | 1.88e+00  |
| 10            | 102   | 6.4   | 1116                  | 7  | S77213 | DNA-directed DNA poly | 1.88e+00  |
| 11            | 101   | 6.3   | 81                    | 7  | C69186 | conserved hypothetica | 2.45e+00  |
| 12            | 66    | 6.2   | 331                   | ~  | S74410 | phenylalaninetRNA l   | 4.11e+00  |
| 13            | 66    | 6.2   | 631                   | ~  | T15370 | hypothetical protein  | 4.11e+00  |
| 14            | 100   | 6.2   | 784                   | ~  | A33633 | transcription repress | 3.18e+00  |
| 15            | 100   | 6.2   | 946                   | ~  | S48397 | hypothetical protein  | 3.18e+00  |
| 16            | 96    | 6.1   | 368                   | ~  | S75923 | sensory transduction  | 5.31e+00  |
| 17            | 98    | 6.1   | 434                   | ~  | S04534 | invasin precursor - Y | 5.31e+00  |
| 18            | 97    | 9.0   | 201                   | 7  | S11799 | pullulanase secretion | 6.85e+00  |
| 19            | 97    | 9.0   | 326                   | Н  | S11921 | pulk protein - Klebsi | 6.85e+00  |
| 20            | 97    | 6.0   | 479                   | 7  | B69764 | transcription regulat | 6.85e+00  |
| 21            | 97    | 9.0   | 482                   | Н  | A34671 | triacylglycerol lipas | 6.85e+00  |
| 22            | 97    | 0.9   | 661                   | 7  | A55877 | 44                    | 6.85e+00  |
| 23            | 97    | 0.9   | 709                   | 7  | S75212 | comE protein - Synech | 6.85e+00  |

A54277 #type complete
transcription adaptor protein p300 - human
#formal\_name Homo sapiens #common\_name man
09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change
20-Sep-1999
A54277
A54277
Eckner, R.; Ewen, M.E.; Newsome, D.; Gerdes, M.; DeCaprio,

ACCESSIONS REFERENCE #authors

RESULT ENTRY TITLE ORGANISM DATE

| hypothetical protein 6.85e+00 hypothetical protein 1.13e+01 probable 181558 trans 1.13e+01 probable 181558 trans 1.13e+01 probable transposase 1.13e+01 probable transposase 1.13e+01 probable transposase 1.13e+01 hypothetical protein 1.13e+01 two-component sensor 1.13e+01 ribonucleoside-diphos 1.45e+01 ribonucleoside-diphos 1.13e+01 ribonucleoside-diphos 1.13e+01 hypothetical protein 1.86e+01 kakapo gene protein 1.86e+01 kakapo gene protein 1.86e+01 groovin gene protein 1.86e+01 | 9 - Ca<br>elega<br>ion 06<br>Librar                                                                      | 505/3 90y #label A 00y #label A 10 | EKVALERIVEQKLAESAKNEKDIAWNVIVVANSYVAKSLRPVINIQMPTVGGDTNFEFD 191 ::                     |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|
| 101239<br>C70937<br>S74659<br>C70936<br>G64836<br>G64828<br>F70678<br>D74115<br>F70000<br>MMBB1<br>A48126<br>B65020<br>S65952<br>S65952<br>G65128<br>G70128<br>G71318                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | comp<br>comp<br>ietn<br>iorha<br>lence<br>EMBL                                                           | y, 1, 2, 1, 1, 1, 2, 1, 2, 1, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,             | CDIAWNVNIV<br> :   ::<br>ADFRWRYDVP                                                    |
| попопопопопопопопопопопопопопопопопопопо                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | #type<br>#type<br>mal pro<br>mal pro<br>ps<br>#seq<br>997<br>to the<br>minary                            |                                                                                        | KNEF<br>:<br>PHV?                                                                      |
| 1111<br>1489<br>1889<br>1889<br>1889<br>1889<br>11139<br>11292<br>11292<br>11292<br>11292<br>11292<br>11292<br>11292<br>11292<br>11292<br>11292<br>11292<br>11293<br>11293<br>11293                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ort # 2001<br>1.02 t M DO 1.00 t C M M M M M M M M M M M M M M M M M M                                   | , o's 5555 5                                                                           | QKLAESAN<br>  :<br> QQ-GAWL <br> L 202<br>  1 200                                      |
| , , , , , , , , , , , , , , , , , , ,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | S4102;<br>hypoth<br>hypoth<br>6+form<br>06-far<br>09-far<br>84101;<br>S4102;<br>S4101<br>S4101<br>Submit | # le # su # le re le co                            | STAGOL<br>STAGOL<br>STAGOL<br>STAGOL<br>STAGOL<br>STAGOL<br>STAGOL<br>STAGOL<br>STAGOL |
| 22222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ໝ່ ຫຼື                                                                                                   | S 1                                                                                    | 132<br>134<br>192<br>192                                                               |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | RE DAR REC                                                                                               | GE SE SU                                                                               | 90 Oy Oy                                                                               |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                          |                                                                                        |                                                                                        |

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#journal Genes Dev. (1994) 8:869-884
#title Molecular cloning and functional analysis of the adenovirus
ElA-associated 300-kD protein (p300) reveals a protein with
properties of a transcriptional adaptor.
#accession A54277
#status
 #authors Meinhardt, L.W.; Krishnan, H.B.; Balatti, P.A.; Pueppke, S.G. #journal Mol. Microbiol. (1993) 9:17-29
#title Molecular cloning and characterization of a sym plasmid locus that regulates cultivar-specific nodulation of soybean by Rhizobium fredil USDA257.
#cross-references MUD:94018604
#accession S35020
 ##residues 1-21/4 ##label ECK
##cross_references GB:U01877; NID:g495300; PIDN:AAA18639.1; PID:g495301
##note in the authors' translation 941-Ser is shown after 961
and consequently, residues 942-961 are displaced one codon to the left
 ñ
 ä
 #superfamily unassigned bromodomain proteins; bromodomain
 84 LSPREFLDRLIDLYDLQWYYDGVVLYVSA-AKEAQTRMLV-LSSVHFSAFKLALDKLDIS 141
 24 LFAGIHTTLGATLPLPSTSYKYTVLDQDLSAALQEFGNNLKISVNISAEVKGRIRGRIPE 83
 S35020 *type complete
nolW protein - Rhizobium fredii
#formal_name Rhizobium fredii
03-Feb-1994 *sequence_revision 03-Feb-1994 *text_change
09-sep-1997
 Gaps
 membrane protein
#length 234 #molecular-weight 25829 #checksum 725
 #domain bromodomain homology #label BRO #length 2414 #molecular-weight 264143 #checksum
 .
8
 ä
 2137 QAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQ-MNMNHNTM-PSQFRDILR 2184
 : |||| |:: |::|| ::|| || || || 65 RDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQ 114
 Score 110; DB 2; Length 2414;
Pred. No. 2.18e-01;
13; Mismatches 18; Indels
 Length 234;
 Query Match 6.8%; Score 109; DB 2; Length 234 Best Local Similarity 27.0%; Pred. No. 2.87e-01; Matches 34; Conservative 35; Mismatches 49; Indels
 heptad repeat; zinc finger
 / Match 6.9%;
Local Similarity 34.0%;
hes 17; Conservative
 ##molecule_type mRNA
 ##molecule_type DNA
 DERYPV 147
 : ||:|
ELRYSV 204
 #map_position
CLASSIFICATION
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1075-1132
SUMMARY
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 REFERENCE
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Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fleids, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fittenman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.B. Thirmann, Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus
 $25768
Wohlfarth, S.; Hoesche, C.; Strunk, C.; Winkler, U.K.
J. Gen. Microbiol. (1992) 138:1325-1335
Molecular genetics of the extracellular lipase of Pseudomonas
 ä
 nucleic acid sequence not shown; translation not shown
 Haemoph11us
 76 ENQIGANLSSNNINNKRLIQLEQSLKTAQENIAQLEQLIVSK--IGEIISLQIQMKQVS 133
 |:|||||:::||
79 EEQLGALLAGMHTLLQQALRLPPTSLK-PDTFRDQLOELCIPQDLVGDLASVYFG-SQRP 136
 ##residues 1-230 ##label TIGR
##cross-references GB:U32742; GB:L42023; NID:g1573593; PID:g1573595;
TIGR:HIO603
:x #length 230 #molecular-weight 25193 #checksum 4558
 134 QL-AIAQQPSDWLFSEADFL--LNNALRKLVLDNDVDTAVSL-LKLADETLVK--VNNSQ 187
uroporphyrin-ii C-methyltransferase homolog - Haemophi
influenzae (strain Rd KW20)
#formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
 Score 108; DB 2; Length 230;
Pred. No. 3.78e-01;
34; Mismatches 56; Indels 10; Gaps
 150 LSAEEKAAAIDRL--RASLPEDQOESVLPQLQSELQOQTAALQAAGAGPEAIRQMRQQL 206
 S25769 #type complete
lipH protein - Pseudomonas aeruginosa
#formal_name Pseudomonas aeruginosa
13.Jan-1995 #sequence_revision 13-Jan-1995 #text_change
07.May-1999
 Gaps
 ##cross-references EMBL:X63391
X #length 283 #molecular-weight 31853 #checksum
 Length 283
 Score 108; DB 2; Length 283
Pred. No. 3.78e-01;
22; Mismatches 16; Indels
 ##molecule_type DNA
##residues 1-283 ##label WOH
 #cross-references MUID:95350630
#accession D64080
 #cross-references MUID:92381478
#accession $25769
 preliminary
 / Match 6.7%;
Local Similarity 27.5%;
hes 38; Conservative
 188 ANEIRSAINQDLKQLLSL 205
 197 FQELRYSVALVLKEMADL 214
 Query Match
Best Local Similarity 30.5%;
Matches 18; Conservative
 ##molecule_type DNA
##residues 1-2:
 D64080
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##molecule_type DNA ##residues 1-33
 ##molecule_type DNA
 Best Local Similarity
Matches 18; Conser
 S24161
 S77558
 S24161
 CLASSIFICATION
 ##status
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 ##residues 1.451 ##label KAN
##cross-references EMBL:D90901; GB:AB001339; NID:g1651897; PID:d1017612;
PID:g1651953
 ##cross-references GB:D26444; NID:g452237; PID:d1006006; PID:g499299
##note the authors translated the codon CCC for residue 236 as
Glu: the authors translated used GTG as an initiation
codon and translated it as Val
the authors say that codon useges suggest this protein
is not expressed at high levels
##ength 451 #molecular-weight 49667 #checksum 7763
 S77558 #type complete
hypothetical protein sll1967 - Synechocystis sp. (strain PCC
6803)
 4
 Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakama, T.; Matuo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of
 the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
 'YDPNLEVAQISNRMLQAGGPGLLFENVKG',
'SPFPVAVNLMGTVERICWAMNMDHPLELEDLGKK', 244-451 ##label
 S74728 #type complete hypothetical protein slr0971 ccmA 3'-region - Synechocystis sp. (strain PCC 6803)
 nucleic acid sequence not shown; translation not shown
 Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
59 LQGEDCRDGVQRLGVSANLPEEQLGALLAGMHT-LLQQALRLPPTSLKPDTFRDQLQEL 116
 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
 Ogawa, T.; Marco, E.; Orus, M.I.
J. Bacteriol. (1994) 176:2374-2378
A gene (ccmA) required for carboxysome formation in
cyanobacterium Synechocystis sp. strain PCC6803.
 42 ALHFDDPRLPEVEQLTLSGT-PEE-LEALALAVETYLQQRLN-PCASLEPSTYPEPV
 4;
 Score 107; DB 2; Length 451;
Pred. No. 4.96e-01;
13; Mismatches 18; Indels
 potential protein-coding regions.
#cross-references MUID:97061201
#accession S74728
 sp. (strain PCC 6803)
#formal_name Synechocystis sp.
 *Iormal_name Synechocystis sp.
 #cross-references MUID:94209239
 6.78;
 Local Similarity 38.6%;
nes 22; Conservative
 21-Aug-1998
S74728; B55214
 26-Aug-1999
 ##molecule_type DNA
##residues 1-45
 ##molecule_type DNA
 A55214
 ##residues
 ##status
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 Query Match
 ##note
 #authors
#journal
 ORGANISM
#variety
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 9
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PID:d1018138;
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 Gaps 10;
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 the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
#superfamily hypothetical protein HI0333
#length 463 #molecular-weight 51523 #checksum 8580
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
fournal
DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of
potential protein-coding regions.
 nucleic acid sequence not shown; translation not shown
 E70805 #type complete
probable mce4 protein - Mycobacterium tuberculosis (strain
H37RV)
 #journal Arch. Biochem. Biophys. (1992) 296:505-513
#title Purification, molecular cloning, and expression of lipase from Pseudomonas aeruginosa.
#cross-references WIDE:9233A4144
 116 RIGGFTTLPLEPLLQSPASL-GYRNKATYP-LSRSKTGQVQAGYYRKGSHRLVNINQCPV 173
 174 QDDRLNLLLTEVKKDIENRGWSIYDEEKKQGKLR-HL-SLRIGQR-TGEMLLTLISAHKG 230
 ##cross-references GB:D10048; NID:g216895; PID:d1001403; PID:g216897
Y #cross-references GB:D10048; NID:g216897
 207 LSTEEKAAAIDRL--RASLPEDQQESVLPQLQSELQQQTAALQAAGAGPEAIRQMRQQL 263
 21 RVS-FLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQGEDCRDGVQRL-GVSA-NL 77
 lipase B - Pseudomonas aeruginosa
#formal_name Pseudomonas aeruginosa
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
 Chihara-Siomi, M.; Yoshikawa, K.; Oshima-Hirayama, N
Yamamoto, K.; Sogabe, Y.; Nakatani, T.; Nishioka,
 Query Match 6.7%; Score 107; DB 2; Length 463; Best Local Similarity 22.3%; Pred. No. 4.96e-01; Matches 31; Conservative 41; Mismatches 57; Indels 10;
 ##residues 1-463 ##label KAN
##cross-references EMBL:D90905; GB:AB001339; NID:g1652360;
PID:g1652483
 Score 106; DB 2; Length 339;
Pred. No. 6.50e-01;
 Indels
 21; Mismatches
 #type complete
 1-339 ##label CHI
 231 LPD-LEEQAGEWLERYPDL 248
 preliminary
 6.6%;
 Conservative
 20-Mar-1998
```

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#start_codon
CLASSIFICATION
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 ##status
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 ##note
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 #authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeler, K.; Gas, S.; Barry III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLen, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Outal, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skalandre, S.; Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
 ##cross-references GB:AL022022; GB:AL123456; NID:g3261554; PID:e1254627;
PID:g2924436
 ##INDAECUARC_IFC L....
##residues 1-1116 ##label KAN
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 #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Watsuno, A.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.; Shimpo, S.; Jakeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Shimpo, S.; Jakeuchi, S.; Jakeuchi, S.; Shimpo, S.; Jakeuchi, S.; Jakeuchi, S.; Shimpo, S.; Jakeuchi, nucleic acid sequence not shown; translation not shown
 126 LSPNAHVAASQV-QLEVNTLFQSLIDLL-HKIDPLETNATLSALSEGLRGHGDDLGALLS 183
 #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
 S77213 #type complete
DNA-directed DNA polymerase (EC 2.7.7.7) III chain dnax
Synechocystis sp. (strain PCC 6803)
protein s111360
 Gaps
 184 GLNTLIRQANPKLP--ALQED-FRKAAVVANVYADAAGDLNTV-FDNLPTINKTIVDQ 237
 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
 #length 400 #molecular-weight 42418 #checksum 124
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 S77213
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 #accession
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REFERENCE
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 #variety
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Smith, D.R.; Doucette-Stamm, L.A.; Deloughery; C.; Lee, H.; Dubols, J.; Aldredge, T.; Basilizzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.; Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire, R.; Warzbowski, J.; Gibson, R.; Jiwahi, N.; Caruso, R.; Bush, D.; Safer, H.; Patvell, D.; Prabhakar, S.; Church, G. M.; Daniels, C.; Goyal, A.; Pietrokovski, S.; Church, G. M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 the EMBL Data
 C69186 *type complete conserved hypothetical protein MTH649 - Methanobacterium thermoautotrophicum (strain Delta H) *formal_iname Methanobacterium thermoautotrophicum 05-Dec-1997 *sequence_revision 05-Dec-1997 *text_change 18-Sep-1998
 576 EEPPERVVFVLAIIDPQ-RVLPIIISRCQRFDYRRIPLQAMVDHLRYIAGRENINIDQPA 634
 635 LTLVAQIANGGLRDAESLLDQ-LSLLPDLITPDKVWD-LVGAVPEQDLLALLEAIASDDA 692
 75 ANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIPQDLVGDLASVVFGSQ 134
 8010
 #title Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis and comparatity genomics.
 #superfamily yeast SNP2 protein
#length 81 #molecular-weight 9061 #checksum 8046
 nucleotidyltransferase
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 shown;
 Length 1116;
the nucleotide sequence was submitted to Library, June 1996
 29; Mismatches 66; Indels
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 C69186
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 355 FATWLACHILE 365
 #map_position
#introns
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 #accession
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 REFERENCE
#authors
#journal
#title
 13
 14
 #authors
 ACCESSIONS
 Matches
 ACCESSIONS
 REFERENCE
 KEYWORDS
SUMMARY
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 ORGANISM
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 SUMMARY
 RESULT
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 catalyzes transfer of activated phenylalanine to
phenylalanyl-tRNA
#supperfamily phenylalanine-tRNA ligase alpha chain
aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
#length 331 #molecular-weight 37124 #checkum 6487
 #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamcto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Markato, A.; Makazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, S.; Tak
 the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 nucleic acid sequence not shown; translation not shown
 S74410 #type complete
phenylalanine--tknka ligase (EC 6.1.1.20) alpha chain -
Synechocystis sp. (PCC 6803)
phenylalanyl-tRNA synthetase alpha chain; protein sl10454
 33 RVQYLGKKGELSLILKGMGKLSAE-ERPKFGAIANEVKEALQHDLESRKANLQNAAIEAQ 91
 115370 #type complete
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20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
20-Sep-1999
 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 16-Jul-1999
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PIDN:BAA10328.1; PID:d1010979; PID:g1001185
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 23; Mismatches 24; Indels
 Johnson, D. submitted to the EMBL Data Library, May 1996 The sequence of C. elegans cosmid C01F1.
 DB 2; Le
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Pred. No. 4
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Best Local Similarity 27.8%;
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 LPEEQLGALLAG 88
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 218338
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 ALTERNATE_NAMES
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 CLASSIFICATION
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 #accession
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#authors
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 TITLE
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 REFERENCE
 KEYWORDS
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Kageyama, R.; Pastan, I.
Cell (1989) 59:815-825
Molecular cloning and characterization of a human DNA binding
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 ##residues 1-946 ##label CHU
##cross-references GB:Z47047; EMBL:Z38059; NID:g603997; PID:g763209;
##CIOSS-references GB:Z471137c
 299 GMITIQLNHLL-IPPNALANETVREQAQQL-IVHELVHQWMGNYISFDS-WESL-WFNES 354
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 #checksum 3428
 848397 #type complete
hypothetical protein YIL137c - yeast (Saccharomyces
 Churcher, C. submitted to the EMBL Data Library, September 1994 $48397
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 5
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α
 Length 784;
 Query Match 6.2%; Score 100; DB 2; Length 946; Best Local Similarity 31.0%; Pred. No. 3.18e+00; Matches 22; Conservative 21; Mismatches 20; Indels
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BD NA binding; transcription regulation
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Best Local Similarity 26.9%;
 14; Conservative
 cerevisiae)
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 ##molecule_type DNA
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 A33633
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 A33633
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::||: |: : . Qy 145 QGAWLP-HVAD 154

Search completed: Fri May 12 10:35:10 2000 Job time : 60 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri May 12 10:36:18 2000; MasPar time 17.97 Seconds 161:524 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-223-796-4 (1-224) from USO9223796.pep 1604 1 MSAVGAATPYLHHPGDSHSG......ALVLKEMADLEKRCERRLQD 224 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

131253 seqs, 12956647 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT\_COMB 4:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 30.751; Variance 151.832; scale 0.203 Statistics:

SUMMARIES

| Pred. No.                | 2.01e-01   | 3.27e-01   | 2.22e+00   | 2.22e+00   | 3.56e+00   | 3.56e+00   | 3.56e+00   | 1.05e+01   | 1.43e + 01 | 1.43e + 01 | 1.43e+01   | 1.43e+01   | 1.43e+01   | 1.43e + 01 | 1.43e+01   | 1.43e+01   | 1.43e + 01 | 2.61e+01   | 2.61e+01   | 2.25e+01   | 3.04e+01   | 3.53e+01   | 3.53e+01   |
|--------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|                          | Applicatio | Applicatio | Applicatio | Applicatio | Applicati  | Applicati  | Applicati  | Applicatio | Applicatio | Applicatio | Applicatio | Applicatio | Applicati  | Applicatio | Applicati  | Applicatio | Applicati  | Applicati  |            |            |            | Applicatio | Applicati  |
| ä                        | 'n         | 7          | 'n         | 'n         | 18,        | 18,        | 31,        | ٦,         | 'n         | 7          | 'n         | 'n         | 10,        | S,         | 10,        | 'n         | 10,        | 17,        | 17,        | 50,        | 55,        | 'n         | 14,        |
| Description              | Sequence   | Sednence   |
| ឧ                        | US-08-822- | US-08-822- | PCT-US95-0 | US-08-227- | US-08-795- | US-08-318- | us-08-576- | US-09-015- | us-09-003- | US-08-357- | PCT-US95-1 | us-09-003- | US-08-357- | PCT-US95-1 | PCT-US95-1 | US-08-357- | US-09-003- | US-08-795- | US-08-318- | US-08-190- | DS-08-576- | US-08-875- | PCT-US95-0 |
| 80                       | 7          | ~          | m          | Ч          | ~          | Н          | ~          | 7          | 7          | П          | m          | 7          | ٦          | m          | ო          | П          | N          | ~          | ч          | -          | ~          | 7          | m          |
| Query<br>Match Length DB | 195        | 195        | 2414       | 2414       | 395        | 395        | 1114       | 448        | 1064       | 1064       | 1064       | 1082       | 1082       | 1082       | 1082       | 1082       | 1082       | 382        | 382        | 603        | 155        | 335        | 350        |
| Query<br>Match           | 7.8        | 7.6        | 6.9        | 6.9        | 6.7        | 6.7        | 6.7        | 6.2        | 6.1        | 6.1        | 6.1        | 6.1        | 6.1        | 6.1        | 6.1        | 6.1        | 6.1        | 5.9        | 5.9        | 5.9        | 5.8        | 5.7        | 5.7        |
| Score                    | 125        | 122        | 110        | 110        | 107        | 107        | 107        | 100        | 86         | 86         | 86         | 86         | 98         | 86         | 86         | 86         | 86         | 94         | 94         | 95         | 93         | 92         | 92         |
| Result<br>No.            | 1          | 7          | m          | 4          | S          | 9          | 7          | 80         | 6          | 10         | 11         | 12         | 13         | 14         | 15         | 16         | 17         | 18         | 19         | 20         | . 21       | 22         | 23         |

| 3.53e+01<br>4.09e+01<br>4.09e+01<br>4.09e+01<br>6.39e+01<br>6.39e+01<br>7.55e+01<br>7.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01<br>8.55e+01                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |            |             |                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| 14, Application 2, Application 3, Application 3, Application 3, Application 108, Application 4, Application 4, Application 4, Application 5, Application 6,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            |             |                  | PROTEIN 2.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| sednence sed                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |            | 195 AA.     |                  | NESIS<br>s, Inc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| US-08-765-<br>US-08-565-<br>US-08-361-<br>US-08-361-<br>US-08-014-<br>US-09-014-<br>US-08-447-<br>US-08-447-<br>US-08-447-<br>US-08-453-<br>US-08-537-<br>US-08-537-<br>US-08-537-<br>US-08-537-<br>US-08-537-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261-<br>US-08-261- | ALIGNMENTS | ; PRT;      | US/08822260      | Dulfer L. K. Timaceutic rive Windows S/08/822, |
| 350<br>476<br>476<br>476<br>476<br>476<br>476<br>476<br>476                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | <b>«</b>   | STANDARD;   | Application US/0 | Application US/088222 583066 NTCOMANTION: NT: Hillman, Jennifer NT: Goli, Surya K. FINVENTION: NOVEL TUM OF SEQUENCES: SSEE: Incyte Pharmaceu SSEE: Incyte Pharmaceu T: 3174 Porter Drive Palo Alto R: CA 94304 R READABLE FORM: M TYPE: DISKette TER: USA 94304 TER: LBM COMPATIBLE TER: LBM COMPATIBLE TER: LBM COMPATIBLE TER: LBM COMPATIBLE TRING SYSTEM: TRING SYSTEM: TRING SYSTEM: TRING SYSTEM: TREE: FastSEG for Windo ARPE: FastSEG for Windo ARPELICATION DATA: CATION NUMBER: US/08/8 G DATE: Herewith PPLICATION DATA: G DATE: TRATTON NUMBER: H DS DE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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| 222<br>222<br>222<br>222<br>222<br>223<br>223<br>223<br>223<br>223                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            | US-08-82    | Sequence         | Sequence Patent General General General General APPI TITH NUMBER SEGUENCE CORRESPONDE SEGUENCE SEGUENC |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | RESU       | gax 8 x e x | (日)              | \$8888888888888888888888888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

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Query Match 7.6%;
Best Local Similarity 24.8%;
Matches 27; Conservative
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 7;
 87 LED-CKFDRERI-ELFCTEYQNNKNSLETLLGSIGRSLPHITDVSWRLEYQIKTNQLHKM 144
 113 LOELC-IPODLVGDLASVVFGSQRPLLDSVAQQQGAWLPHVADFRWRVDVAISTSALARS 171
 Gaps
 7;
 Score 125; DB 2; Length 195;
Pred. No. 2.01e-01;
37; Mismatches 40; Indels
 145 YRPGYLVTLNVENNDSQSYPEINFSCNMEQLQDLVG-KLKDASKSLER 191
 APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL TUMORIGENESIS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,260
 195 AA
 FILING DATE: Herewith CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,740
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
 TOPOLOGY: Iinear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 265569
JENCE 195 AA; 22037 MW; 190094 CN;
 TOPOLOGY: linear
IMMEDIATE SOURCE:
LIEBRARY: UTRSNOT02
CLONE: 2267574
ENCE 195 AA; 22151 MW; 196728 CN;
 PRT;
 Sequence 1, Application US/08822260
Patent No. 5830660
GENERAL INFORMATION:
 Sequence 1, Application US/08822260
 SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDEDNESS: single
 STANDARD;
 INFORMATION FOR SEQ ID NO:
 TELEFAX: 415-845-4166
STRANDEDNESS: single
 Query Match 7.8%;
Best Local Similarity 22.2%;
Matches 24; Conservative
 USA
 94304
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 JT 2
US-08-822-260-1
 COUNTRY:
 CITY: F
 SEQUENCE
 SEQUENCE
 XXXXX
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 87 LED-CKFDRERI-ELFCTEYQNNKNSLEILLGSIGRSLPHITDVSWRLEYQIKTNQLHRM 144
 Gaps
 Gaps
 6
 Score 110; DB 3; Length 2414;
Pred. No. 2.22e+00;
13; Mismatches 18; Indels 2;
 NUCLEIC ACID ENCODING TRANSCRIPTION
FACTOR P300 AND USES OF P300
13
 2137 QAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQ-MNMNHNTM-PSQFRDILR 2184
 : |||| |:: |::|| ::|| 65 RDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQ 114
Score 122; DB 2; Length 195;
Pred. No. 3.27e-01;
35; Mismatches 38; Indels
 145 YRPAYLVTLSVQNTDSPSYP-EISFSCSMEQLQDLVG-KLKDASKSLER 191
 ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
 SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04682 FILING DATE:
 2414 AA.
 CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DUADA:
APPLICATION NUMBER: US 08/227,536
FILING DAIE: 14-April-1994
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: HOlliday C. Heine, Ph.D.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCI-308Xq999
TELEPHONE: (617) 542-2290
TELEPHONE: (617) 451-0313
INFORMATION FOR SEQ 1D NO: 2:
 LE TYPE: protein
2414 AA; 264143 MW; 29411911 CN;
 PRT;
 Sequence 2, Application PC/TUS9504682
GENERAL INFORMATION:
APPLICANT:
 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 2, Application PC/TUS9504682
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
LENGTH: 2414 amino acids
TYPE: amino acid
 STANDARD;
 TITLE OF INVENTION: NU
TITLE OF INVENTION: FA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 Query Match 6.9%;
Best Local Similarity 34.0%;
Matches 17; Conservative
 linear
 S
 TOPOLOGY: 1
 COUNTRY: US
 3
ID PCT-US95-04682-2
XX
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 SEQUENCE
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180 ELIPENAEAVARFLGDAVDREP-ALMLEYFCRCAREESKRVPPRIFGSAPRLTEDDFGLL 238
 Sequence 18, Application US/08318947A
Patent No. 5798345
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
APPLICANT: Tian, Qingsheng
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
 TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: Z100 Pennsylvania Avenue, NW Suite 800 CITY: Washington
 Score 107; DB 2; Length 395;
Pred. No. 3.56e+00;
25; Mismatches 33; Indels
 STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,303
FILING DATE: 04-FEB-1997
CLASSIFICATION NUMBER: 08/318,947
FILING DATE: 07-0CT-1993
ATONREY/AGENT INFORMATION:
NAME: MACK, SUSAN J.
REGISTRATION NUMBER: 30,951
REFERENCE/POCKET NUMBER: 30,951
REGISTRATION NUMBER: 30,951
REGISTRATION NUMBER: 30,951
REGISTRATION INFORMATION:
TELECOMMULICATION INFORMATION:
TEL
 2: Sughrue, Mion, Zinn, Macpeak & Seas
2100 Pennsylvania Avenue, NW Suite 800
 395 AA
 PRT;
 239 NTALAEMRRICLDLPPVP--PNAYTPYHLRE 267
 SE LAGMHTLLQQALRLPPTSLKPDTFRD-QLQE 115
 MOLECULE TYPE: protein
FENCE 395 AA; 42522 MW; 753192 CN;
 Sequence 18, Application US/08318947A
 TELEFAX: (202)293-2920
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
 STANDARD;
 : 395 amino acids
amino acid
 Query Match 6.7%;
Best Local Similarity 29.7%;
Matches 27; Conservative
 linear
 CITY: Washington
 US-08-318-947A-18
 TOPOLOGY:
 STREET:
 SEQUENCE
 XXXXXX
 RESULT
 å
 ñ
 Gaps
 Sequence 2, Application US/08227536
Patent No. 5658784
GENERAL INFORMATION:
APPLICANT: ECKNET, Richard
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
UNDABRE OS SEQUENCES: 13
CORRESPONDENCE ADDRESS:
 ;
;
 Sequence 18, Application US/08795303
Patent No. 5948656
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
APPLICANT: Tan, Qingsheng
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
 2137 QAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQ-MNMNHNTM-PSQFRDILR 2184
 Score 110; DB 1; Length 2414;
Pred. No. 2.22e+00;
13; Mismatches 18; Indels 2
 : |||| |:: |::|| :::|
65 RDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLRPDTFRDQLQ 114
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,536
FILING DATE: 14-APR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/COCKET NUMBER: 34,380
REFERENCE/COCKET NUMBER: 34,380
TELEBOMUNICATION INFORMATION:
TELECOMMUNICATION 110FORMATION:
TELEBOMMINICATION 1500 2:
SEQUENCE CRARACTERISTICS:
LENGTH: 2414 amino acids
 ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
 2414 AA.
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 395
 MOLECULE TYPE: protein
JENCE 2414 AA; 264143 MW; 29411911 CN;
 PRT;
 PRT;
 Sequence 18, Application US/08795303
 Sequence 2, Application US/08227536
 STANDARD;
 STANDARD;
 Query Match 6.9%;
Best Local Similarity 34.0%;
Matches 17; Conservative
 linear
 COUNTRY: US
ZIP: 02109
 RESULT 5
ID US-08-795-303-18
 STATE: MA
RESULT 4
ID US-08-227-536-2
 SEQUENCE
 XXXXXX
 XXXXXX
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6; Gaps

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LOCATION: (1)..(446)
OTHER INFORMATION: PROTEIN KINASE DOMAIN OF ICP10 SUBUNIT OF HSV-2
 150 MTAVLGAAGVLR--GAAWDARVS-LDAQLSPQQLAVTEAAVAALPADPALRAL-FAGAEM 205
 206 TANTVVDAVLAVSAEPGLAE-RIADDPAAAQRTVAEVLRLHPA-LHLER-RTATAEVRLG 262
 Gaps
 APPLICANT: AURELIAN, LAURE
APPLICANT: SMITH, CYNTHIA
TITLE OF INVENTION: HERPES SIMPLEX VIRUS TYPE SPECIFIC SEROASSAY
FILTE PEFFRENCE: 1437LA
CURRENT MPPLICATION NUMBER: US/09/015,815
CURRENT FILING DATE: 1998-01-29
EARLIER PEPLING DATE: 1997-01-31
NUMBER: OS SEQ ID NOS: 1
SOFTWARE: PATENTIN VET: 2.0
 æ
;
 Score 107; DB 2; Length 1114;
Pred. No. 3.56e+00;
36; Mismatches 54; Indels
 448 AA.
 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY, AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857.US.O1
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
 TOPOLOGY: linear
MOLECULE TYPE: No. 5998194e
FENCE 1114 AA; 120173 MW; 5916545 CN;
 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
 PRT;
 Sequence 1, Application US/09015815
Patent No. 5965356
GENERAL INFORMATION:
 ORGANISM: herpes simplex virus-2 FEATURE:
 Sequence 1, Application US/09015815
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1114 amino acids
TYPE: amino acid
STRANDEDNESS: single
 STANDARD;
 Match 6.7%;
Local Similarity 25.2%;
les 33; Conservative
 263 EHVIGEGEEVV 273
 120 ODLVGDLASVV 130
 NAME/KEY: DOMAIN
 US-09-015-815-1
 SEQ ID NO 1
LENGTH: 448
 TYPE: PRT
 SEQUENCE
 Query Match
 XXXXXX
 Matches
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 180 ELIPENAEAVARFLGDAVDREP-ALMLEYFCRCAREESKRVPPRTFGSAPRLTEDDFGLL 238
 Score 107; DB 1; Length 395;
Pred. No. 3.56e+00;
25; Mismatches 33; Indels 6; Gaps
 CAPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bub PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,947A
FILING DATE: 06-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,951
REFERENCE/DOCKET NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELEPHONE: (202)293-7060
TELEPHONE: (202)293-7060
TELEPHONE: (202)293-7060
TELEPHONE: 395 and no caids
TYPE: and no caids
TYPE: and no caids
 Sequence 31, Application US/08576626A
Patent No. 5998194
GENERAL INFORMATION:
APPLICANT: Summers, R.G.
APPLICANT: Staver, L.
APPLICANT: Staver, L.
APPLICANT: Staver, W.J.YETIDE-ASSOCIATED SUGAR TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR TITLE OF INVENTION: BIOSYNTHESIS GENES NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: ALO Abbott Park Road
 1114 AA.
 PRT;
 86 LAGMHTLLQQALRLPPTSLKPDTFRD-QLQE 115
 239 NTALAEMRRLCLDLPPVP--PNAYTPYHLRE 267
 TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 395 AA; 42522 MW; 753192 CN;
 Sequence 31, Application US/08576626A
 COUNTRY: USA
ZIF: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
 STANDARD;
 Query Match 6.7%;
Best Local Similarity 29.7%;
Matches 27; Conservative
 CITY: Abbott Park
STATE: Illinois
 RESULT 7
AC XXXXXX
AC XXXXXX
DT XX
DT XX
C Sequence 31, Applic:
XX Sequence APPLICANT: State
XX APPLICANT: State
XX APPLICANT: State
XX SEQUENCE
XX STREET: 100
XX STREET: 100
XX STREET: 101
XX STREET:
STATE: USE COUNTRY: USE 20037
 SEQUENCE
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74 ATEDLSCWFPRATSSPWRM 92
 linear
 TELEPHONE:
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US-08-357-598-2
 TOPOLOGY:
MOLECULE TY:
 SEQUENCE
 XXXXX
 RESULT
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 324 ELIPENAEAVARFLGDAVDREP-ALMLEYFCRCAREESKRVPPRIFGSAPRLTEDDFGLL 382
 6; Gaps
 Sequence 2, Application US/09003289
Patent No. 5916792
GENERAL INFORMATION:
APPLICANT: CIVIN, Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 14225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
 Length 448;
 24; Mismatches 34; Indels
 COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,289
 1064 AA.
 Score 100; DB 2;]
Pred. No. 1.05e+01;
 07265/033001
 APPLICATION NUMBER: US/08/357,598
FILING DATE: 15-DEC-1994
ATORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/03300
TELEPROMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 :: : : | ||| : |:: :|:| 86 LAGMHTLLQQALRLPPTSLKPDTFRD-QLQE 115
 383 NYALAEMRRICLDLPPVP--PNAYTPYHLRE 411
 448 AA; 46940 MW; 974341 CN;
 PRT;
 Sequence 2, Application US/09003289
 : 1064 amino acids
amino acid
 STANDARD;
 CLASSIFICATION:
PRIOR APPLICATION DATA:
 Query Match 6.2%;
Best Local Similarity 29.7%;
Matches 27; Conservative
 PUBLICATION INFORMATION:
AUTHORS: NELSON ET AL.,
JOURNAL: J. Biol. Chem.
UBLICATION INFORMATION:
 AUTHORS: CHUNG ET AL., JOURNAL: J. Virol.
 PAGES: 17021-17027
DATE: 1996
 PAGES: 3389-3398
DATE: 1989
 FILING DATE:
 US-09-003-289-2
 SEQUENCE
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 19 LSTEAGALHVLLPARGPGPPQRL-SFSFGDHLAEDLCVQAAKASAILPV-Y--H-SLFAL 73
 19 LSTEAGALHVLLPARGPGPPQRL-SFSFGDHLAEDLCVQAAKASAILPV-Y--H-SLFAL 73
 6; Gaps
 ġ
 GENERAL INFORMATION:
APPLICANT: Clvin, Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
 Query Match 6.1%; Score 98; DB 1; Length 1064; Best Local Similarity 22.8%; Pred. No. 1.43e+01; Matches 18; Conservative 26; Mismatches 29; Indels
 Score 98; DB 2; Length 1064;
Pred. No. 1.43e+01;
26; Mismatches 29; Indels
 COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,598
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07.265/033001
TELECOMMUNICATION INFORMATION:
 MOLECULE TYPE: protein
FENCE 1064 AA; 118717 MW; 5778568 CN;
MOLECULE TYPE: protein
SEQUENCE 1064 AA; 118717 MW; 5778568 CN;
 PRT;
 Sequence 2, Application US/08357598
Patent No. 5705625
 Sequence 2, Application US/08357598
 1064 amino acids
 : 619/678-5070
619/678-5099
 TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 STANDARD;
 ::: : |:|: ||:
141 VAQQQGAWLPHVADFRWRV 159
 74 ATEDLSCWFPRATSSPWRM 92
 Query Match 6.1%;
Best Local Similarity 22.8%;
Matches 18; Conservative
 amino acid
 linear
 STATE: CA
COUNTRY: USA
ZIP: 92037
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XXXXXX

RESULT

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82 IGALLAGMHTLLQQALRLPPTSLKPDTFRDQL-QELCIPQDLVGDLASVVFGSQRPLLDS 140
 19 LSTEAGALHVLLPARGPGPPQRL-SFSFGDHLAEDLCVQAAKASAILPV-Y--H-SLFAL 73
 Score 98; DB 2; Length 1082;
Pred. No. 1.43e+01;
26; Mismatches 29; Indels 6;
 GENERAL INFORMATION:
APPLICANT: C1v1n, Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
 Sequence 10, Application US/08357598
Patent No. 5705625
GENERAL INFORMATION: Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
 SOFTWARE: Patentin Release #1.0, Version #1.30
 ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/357,598
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
RECISTARTION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/033001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE 619/678-5070
 MOLECULE TYPE: protein
FENCE 1082 AA; 120714 MW; 5959860 CN;
 LENGTH: 1082 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5916792 Relevant
 PRT;
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003, 28
 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 Sequence 10, Application US/08357598
 TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 STANDARD;
 141 VAQQQGAWLPHVADFRWRV 159
 // Match
Local Similarity 22.8%;
Local Similarity 22.8%;
Les 18; Conservative
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 74 ATEDLSCWFPRATSSPWRM 92
 COMPUTER: IBM PC
OPERATING SYSTEM:
 linear
 USA
 FILING DATE:
 S
 US-08-357-598-10
 COUNTRY:
 SEQUENCE
 Query Match
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Matches
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 19 LSTEAGALHVLLPARGPGPPQRL-SFSFGDHLAEDLCVQAAKASAILPV-Y--H-SLFAL 73
 6; Gaps
 Sequence 2, Application PC/TUS9516435
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
 Score 98; DB 3; Length 1064;
Pred. No. 1.43e+01;
26; Mismatches 29; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 1064 AA.
 1082 AA.
 MOLECULE TYPE: protein
SEQUENCE 1064 AA; 118717 MW; 5778568 CN;
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16435
FILING DATE: 15-DEC-1995
CLASSIFICATION:
 PRT;
 PRT;
 Sequence 2, Application PC/TUS9516435
 Sequence 5, Application US/09003289
Patent No. 5916792
 ATTORNEY/AGENT INFORMATION:
NAME: HAILe, ilsa A.
REGISTRATION NUMBER: 9726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5079
 Sequence 5, Application US/09003289
 TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 amino acids
TYPE: amino acid
TOPOLOGY: 11near
 STANDARD;
 STANDARD;
141 VAQQQGAWLPHVADFRWRV 159
 74 ATEDLSCWFPRATSSPWRM 92
 f Match
Local Similarity 22.8%;
hes 18; Conservative
 CA
USA
 COUNTRY: U
 RESULT 12
XX
AC XXXXXX
XX
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DT
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DE Sequence 5, Appl1
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CC Sequence 5, Appl1
CC Patent No. 59167
 JT 11
PCT-US95-16435-2
 Query Match
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JAK3

1082 AA.

Matches

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19 LSTEAGALHVLLPARGPGPPQRL-SFSFGDHLAEDLCVQAAKASAILPV-Y--H-SLFAL 73
 Sequence 10, Application PC/TUS9516435
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
 Length 1082;
 Score 98; DB 3; Length 1082; Pred. No. 1.43e+01; 26; Mismatches 29; Indels
 MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16435
FILING DATE: 15-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile. 15-DEC-1995
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
 1082 AA.
 07265/033WO1
 MOLECULE TYPE: protein
SEQUENCE 1082 AA; 120714 MW; 5959860 CN;
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 1082 AA; 120714 MW; 5959860 CN;
 PRT;
 Sequence 10, Application PC/TUS9516435
 REGISTRATION NUMBER: 38,347
REPRENCE/POCKET NUMBER: 07266
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5079
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1082 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
 STRANDEDNESS: not relevant
TOPOLOGY: linear
 SEQUENCE CHARACTERISTICS:
LENGTH: 1082 amino acids
TYPE: amino acid
 STANDARD;
 STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
 141 VAQQQGAWLPHVADFRWRV 159
 / Match 6.1%;
Local Similarity 22.8%;
les 18; Conservative
 74 ATEDLSCWFPRATSSPWRM 92
 JT 15
PCT-US95-16435-10
 Query Match
 XXXXXX
 Matches
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 19 LSTEAGALHVLLPARGPGPPQRL-SFSFGDHLAEDLCVQAAKASAILPV-Y--H-SLFAL 73
 6; Gaps
 Sequence 5, Application PC/TUS9516435
GENERAL INFORMATION:
GENERAL INFORMATION:
FOR INFORMATION:
NUMBER OF INVENTION:
NUMBER OF SEQUENCES: 12
CORRESPONDENCE: 12
CORRESPONDENCE: 12
CORRESPONDENCE: F18h & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: F10ppy disk
COMPUTER: F10ppy disk
COMPUTER: F10ppy disk
COMPUTER: PATEMENT POSS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CORRENT A
 Score 98; DB 1; Length 1082;
Pred. No. 1.43e+01;
26; Mismatches 29; Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,598
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/033001
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1082 amino acids
"VEDER TO THE TO
 1082 AA.
 MOLECULE TYPE: protein
JENCE 1082 AA; 120714 MW; 5959860 CN;
 APPLICATION NUMBER: PCT/US95/16435
FILING DATE: 15-DEC-1995
 PRT;
 Sequence 5, Application PC/TUS9516435
 TYPE: amino acid
STRANDEDNESS: not relevant
 FILING DATE: 15-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
 STANDARD;
 ::: : |:|: ||:
141 VAQQQGAWLPHVADFRWRV 159
 74 ATEDLSCWFPRATSSPWRM 92
 / Match 6.1%;
Local Similarity 22.8%;
nes 18; Conservative
 linear
STATE: CA
COUNTRY: USA
92037
 T 14
PCT-US95-16435-5
 SEQUENCE
 Query Match
 XXXXXX
 Matches
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ŝ
Query Match 6.1%; Score 98; DB 3; Length 1082;
Best Local Similarity 22.8%; Pred. No. 1.43e+01;
Matches 18; Conservative 26; Mismatches 29; Indels 6; Gaps
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74 ATEDLSCWFPRATSSPWRM 92 :::: |:|:: ||: 141 VAQQQGAWLPHVADFRWRV 159

Search completed: Fr1 May 12 10:36:40 2000 Job time : 22 secs.

| ******                                  | (TM)    |
|-----------------------------------------|---------|
| *******                                 |         |
| *************************************** |         |
| ********                                |         |
| *****                                   |         |
| *****                                   |         |
| ******                                  | [====== |
| ******                                  |         |
| * * * *                                 |         |

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri May 12 10:35:27 2000; MasPar time 29.93 Seconds 177.250 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-223-796-4 (1-224) from USO9223796.pep 1604 1 MSAVGAATPYLHHPCDSHSG......ALVLKEMADLEKRCERRLQD 224

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

a-geneseq36 1:geneseqp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 33.179; Variance 157.131; scale 0.211

### SUMMARIES

| Pred. No.      | 1.42e-104              | 6.45e-01               | 6.45e-01               | 1.72e+00               | 1.72e+00               | 1.72e+00               | 1.72e+00               | 4.50e+00               | 4.50e+00               | 4.50e+00               | 7.24e+00               | 7.24e+00               | 8.48e+00               | 8.48e+00               | 1.16e+01          | 2.16e+01               | 2.16e+01               | 2.16e+01 | 2.16e+01 | 2.16e+01               | 2.94e + 01             | 4.65e+01               | 5.41e+01               |
|----------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-------------------|------------------------|------------------------|----------|----------|------------------------|------------------------|------------------------|------------------------|
| Description    | Rat Hypertension relat | Amino acid sequence of | Human secreted protein | Human Zneul partial po | Human Zneul partial po | Human neuro-growth fac | Human neuro-growth fac | Transcription factor p | Transcription factor p | Cellular transcription | Sugar blosynthesis enz | S.erythraea dTDP-4-ket | Protein activated lipa | Human VRRP-1 (VR2) cap | Lipase modulator. | DNA-binding protein GC | Human GC binding prote |          |          | HSV-2 strain SB5 Conti | Protein tyrosine kinas | WD-40 domain-contg. ra | Sequence of herpes sim |
| Ωī             | W37723                 | W71684                 | X07867                 | W88390                 | W88391                 | W88382                 | W88381                 | R84883                 | R84882                 | W40057                 | W19734                 | W99387                 | R77317                 | W99798                 | R47213            | R04107                 | W34179                 | W72206   | W72020   | W72098                 | R96037                 | R85889                 | P71182                 |
| 80             | ч                      | П                      | ٦                      | -                      | -                      | -                      | Н                      | Н                      | Н                      | Н                      | Н                      | Н                      | ~1                     | Н                      | Н                 | ٦                      | Н                      | Н        | Н        | Н                      | Н                      | Н                      | -                      |
| Length         | 224                    | 195                    | 196                    | 169                    | 181                    | 254                    | 273                    | 800                    | 2414                   | 2414                   | 360                    | 361                    | 339                    | 727                    | 344               | 694                    | 784                    | 1144     | 1180     | 1180                   | 1064                   | 603                    | 1137                   |
| Query<br>Match | 82.2                   | 7.6                    | 7.6                    | 7.2                    | 7.2                    | 7.2                    | 7.2                    | 6.9                    | 6.9                    | 6.9                    | 6.7                    | 6.7                    | 9.9                    | 9.9                    | 6.5               | 6.2                    | 6.2                    | 6.2      | 6.2      | 6.2                    | 6.1                    | 5.9                    | 5.9                    |
| Score          | 1319                   | 122                    | 122                    | 116                    | 116                    | 116                    | 116                    | 110                    | 110                    | 110                    | 101                    | 107                    | 106                    | 106                    | 104               | 100                    | 100                    | 100      | 100      | 100                    | 98                     | 95                     | 94                     |
| Result<br>No.  | 1                      | 7                      | m                      | 4                      | 2                      | 9                      | 7                      | 80                     | 6                      | 10                     | 11                     | 12                     | 13                     | 14                     | 15                | 16                     | 17                     | 18       | 19       | 20                     | 21                     | 22                     | 23                     |

| 6.29e+01              | 6.29e+01              | 7.31e+01              | 7.31e+01               | 7.31e+01               | 8.49e+01               | 8.49e + 01             | B.49e+01               | 8.49e+01               | 8.49e+01               | 8.49e+01               | 8.49e+01               | 8.49e+01               | 9.86e+01               | 9.86e+01            | 1.14e+02              | 1.33e+02               | 1.14e+02               | 1.14e+02               | 1.14e+02               | 1.14e+02              | 1.33e+02               |
|-----------------------|-----------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|---------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|
| Entamoeba histolytica | Entamoeba histolytica | Pseudomonas sp. SD705 | Human liver activin be | Human growth different | Wheat adenylosuccinate | Arabidopsis adenylosuc | Arabidopsis adenylosuc | Arabidopsis adenylosuc | Human OC-116 kDa prote | Cellulose synthase ope | Acetobacter xylinum bc | Sed ID #8 from DE19653 | Mutant prenyl diphosph | Human hSK1 protein. | H. pylori transporter | Human secreted protein | Defective tyrosine kin | Saccharomyces cerevisi | Protein kinase (HRR25) | H. pylori transporter | RING11 antigenic pepti |
| R68975                | R70681                | R99975                | W60619                 | R92754                 | W02616                 | W99454                 | R97733                 | W02614                 | W41943                 | R45002                 | W69758                 | W64232                 | W52284                 | W63701              | W20289                | W74908                 | R31888                 | R76615                 | R56519                 | W20640                | R25591                 |
| -4                    | Н                     | ٦                     | Н                      | m                      | н                      | Н                      | Н                      | Н                      | Н                      | Н                      | Н                      | Н                      | H                      | ч                   | Н                     | Н                      | Н                      | Н                      | н                      | Н                     | Н                      |
| 1291                  | 1292                  | 335                   | 350                    | 350                    | 476                    | 490                    | 490                    | 490                    | 822                    | 1319                   | 1326                   | 1336                   | 332                    | 561                 | 182                   | 279                    | 464                    | 464                    | 494                    | 519                   | 989                    |
| 5.8                   | 5.8                   | 5.7                   | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.6                    | 5.6                 | 5.5                   | 5.5                    | 5.5                    | 5.5                    | 5.5                    | 5.5                   | 5.5                    |
| 93                    | 93                    | 92                    | 85                     | 92                     | 91                     | 91                     | 91                     | 91                     | 91                     | 91                     | 91                     | 91                     | 8                      | 06                  | 88                    | 88                     | 88                     | 88                     | 89                     | 89                    | 88                     |
| 24                    | 25                    | 26                    | 27                     | 28                     | 29                     | 30                     | 31                     | 32                     | 33                     | 34                     | 35                     | 36                     | 37                     | 38                  | 39                    | 40                     | 41                     | 42                     | 43                     | 44                    | 45                     |
|                       |                       |                       |                        |                        |                        |                        |                        |                        |                        |                        |                        |                        |                        |                     |                       |                        |                        |                        |                        |                       |                        |

## ALIGNMENTS

|   |                    |                           |                                                                                                                     |                                      |                                      |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    |                 |                                             |                                          |             |                                                                     |                                                                     |         |                                                                    |                                                    | ž.                                                                                                                             | i                                 |          |             | ő                                           |                                                              |     |                                                              | 0                                                            |
|---|--------------------|---------------------------|---------------------------------------------------------------------------------------------------------------------|--------------------------------------|--------------------------------------|-----------------------------------------|---------------------|-----------------|----------------------------|------|--------------|------|-------------|--------------|----------|--------------|--------------------|-----------------|---------------------------------------------|------------------------------------------|-------------|---------------------------------------------------------------------|---------------------------------------------------------------------|---------|--------------------------------------------------------------------|----------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|-----------------------------------|----------|-------------|---------------------------------------------|--------------------------------------------------------------|-----|--------------------------------------------------------------|--------------------------------------------------------------|
|   |                    |                           | 7                                                                                                                   | ì                                    |                                      |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    |                 |                                             |                                          |             | E                                                                   | id.                                                                 |         | ω                                                                  |                                                    | cancer,                                                                                                                        |                                   |          |             | sd                                          | 9                                                            |     | 9                                                            | 120                                                          |
|   |                    |                           | ,                                                                                                                   | į                                    |                                      |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    |                 | Ω                                           |                                          |             | 101                                                                 | yro                                                                 | tio     | lat                                                                |                                                    |                                                                                                                                |                                   |          |             | Gaps                                        | ALH                                                          |     | $_{ m SIO}$                                                  | IPQ                                                          |
|   |                    |                           | Rat Hypertension related calcium regulator.<br>Hypertension related calcium regulated gene. HoaRG: rat parathyroid: |                                      | stroke;                              |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    | •               | develop                                     |                                          |             | This is the amino acid sequence of the hypertension related calcium | regulated gene (HCaRG), which was isolated from the rat parathyroid | tra     | An antibody against the protein, can be used to detect or modulate | 5                                                  | specifically be used to detect or treat, e.g. nypertension,<br>hyperthyroidism, osteoporosis, heart failure, diabetes, stroke, |                                   |          |             | ő                                           | MSALGAAAPYLHHPADSHSGRVSFLGSOPSPEVTAVAOLLKDLDRSTFRKLLKLVVGALH |     | MSAVGAATPYLHHPGDSHSGRVSFLGAQLPPEVAAMARLLGDLDRSTFRKLLKFVVSSLQ | GKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQ |
|   |                    |                           | 2                                                                                                                   | ioi                                  | str                                  |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    |                 |                                             |                                          |             | ated                                                                | par                                                                 | cen     | 77.                                                                | Trey can                                           | str                                                                                                                            | ,                                 |          | 224;        | m                                           | (LKI                                                         | Ξ   | CLKE                                                         | EELC                                                         |
|   |                    |                           | 4                                                                                                                   | tens                                 | es;                                  |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    |                 | <u>د</u> د                                  | ke,                                      |             | rela                                                                | rat                                                                 | 8       | o t                                                                | Lue                                                | ens.                                                                                                                           | Ì                                 |          | 감           | Indels                                      | FRK                                                          | Ξ   | FRK                                                          | AFQ                                                          |
|   |                    |                           |                                                                                                                     | hypertension;                        | diabetes;                            |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    | ,               | ful                                         | Stroke,                                  | י<br>מ<br>מ | uo                                                                  | he                                                                  | T rum   | ete                                                                | . 1                                                | bet                                                                                                                            |                                   |          | Length 224; | ı H                                         | RST                                                          | Ξ   | RST                                                          | KPD                                                          |
|   |                    |                           | קני                                                                                                                 | À                                    |                                      |                                         |                     |                 |                            |      |              |      |             |              |          |              |                    |                 | - useful to                                 | ertension, stroke,<br>Atabates or asthma | 3           | isus                                                                | Ĕ                                                                   | alc     | 9                                                                  | (e.g. ennance or innibit) abnormal calcium levels. | dia                                                                                                                            |                                   |          |             | 04;                                         | KDLL                                                         | Ξ   | SDL                                                          | PASI                                                         |
|   |                    |                           |                                                                                                                     | ody;                                 | e)                                   |                                         |                     |                 | =                          |      |              |      |             |              |          | ٦<br>;       |                    |                 | 0 6                                         | STOI                                     | ני<br>ני    | erte                                                                | fro                                                                 | ar<br>O | ed t                                                               | ě,                                                 | 5                                                                                                                              | ì                                 |          | B 1,        | e-1(<br>s                                   | OLLI                                                         | =   | RLLC                                                         | RLPI                                                         |
|   |                    |                           | tor                                                                                                                 | antibody;                            | failure;                             |                                         |                     |                 | tif                        |      |              |      |             |              |          |              |                    |                 | gen                                         | Ten                                      | 200         | hyp                                                                 | ted                                                                 | lul     | Sn.                                                                | ביין<br>ביין                                       | 110                                                                                                                            | <br>                              |          | Ω           | .42<br>che                                  | AVA                                                          | -:  | AMA                                                          | OAL                                                          |
| ı |                    |                           | ula                                                                                                                 | a a                                  |                                      | <u>:</u>                                |                     |                 | e<br>a                     |      |              |      |             |              |          | Tremblay     |                    |                 | g                                           |                                          | 3           | he                                                                  | ola                                                                 | cel     | pe .                                                               | arc                                                | eat                                                                                                                            |                                   |          | 319;        | omat                                        | EVI                                                          | =   | EVA                                                          | LLC                                                          |
|   |                    |                           | reg                                                                                                                 | 101                                  | sart                                 |                                         | SIS                 | :               | 11ke                       |      |              |      |             |              |          | Tre          |                    |                 | ılat<br>L                                   | i i                                      | , de        | 4                                                                   | 15                                                                  | Ktra    | car                                                                | T 1                                                | r ti                                                                                                                           |                                   |          | 1           | M. M.                                       | OPSI                                                         | i   | OLPI                                                         | GTHI                                                         |
|   | AA.                |                           | calcium regulator.                                                                                                  | extracellular calcium concentration; | hyperthyroidism; osteoporosis; heart | initammatory disease; astruma<br>attus. | Location/Qualifiers | i               | /note= "EF-hand like motif |      |              |      |             |              |          | ď            |                    |                 | Hypertension related calcium regulated gene | e.g. nypertension,                       | 200         | 90                                                                  | ¥.                                                                  | ج<br>و  | in,                                                                | er o                                               | ρĒ                                                                                                                             | inflammatory disease, and asthma. |          | COL         | Pred. No. 1.42e-104;<br>33; Mismatches 13;  | TGS                                                          | =   | TGA                                                          | LLA                                                          |
|   | 224                |                           | alc                                                                                                                 | ent                                  | Sis                                  | :se:                                    | ua]                 |                 | -ha                        |      |              |      |             |              |          | zuk          |                    |                 | ٩,                                          |                                          | i G         | nen                                                                 | ich                                                                 | ğ       | ote                                                                | app                                                | stec                                                                                                                           | ast                               |          |             |                                             | VSF                                                          | Ξ   | <b>VSE</b>                                                   | ZLAV                                                         |
|   | ,<br>E             | cry)                      | D 7                                                                                                                 | 000                                  | Sor                                  | 1560                                    | 2<br>Vuc            | _ [             | E                          |      |              |      |             |              |          | vanc         | •                  | Ì               | alci                                        | detect,                                  | 1091        | Sec                                                                 | ×                                                                   | late    | E D                                                                | ֝֟֝֟֝֟֝֟֝֓֓֓֓֓֓֓֓֓֟֝֟֝֓֓֟֝֟֝֓֓֓֟֝֟֝֟֝ <u>֚֚</u>    | o d                                                                                                                            | and                               |          | .28         | 79.5%;<br>rative                            | HSGI                                                         |     | HSGI                                                         | SEE                                                          |
|   | standard; Protein; | 09-JUN-1998 (first entry) | late                                                                                                                | , <b>5</b>                           | teol                                 | >₁<br>g                                 | atic                | 1521            | te                         |      | CA0439.      | 495  |             |              |          | P, Lewanczuk |                    |                 | υi<br>U                                     | products to treat or detect,             | 7:0         | cid                                                                 | RG)                                                                 | egu     | Ť.                                                                 | מנו                                                | t d                                                                                                                            | (a)                               |          | 82          | larity 79.5%<br>Conservative                | ADS                                                          | =   | GDS                                                          | ANL                                                          |
|   | Pr                 | rst                       | re                                                                                                                  | 101                                  | SO                                   | LOI                                     | Š                   | 12.             | ou/                        |      | 439          | 667  | ·<br>·      | LEWANCZUK R. | ה        | ď            | 7                  |                 | ate                                         | products to treat or                     | 1 - 9       | . G                                                                 | HCa                                                                 | S.      | nst                                                                | 1                                                  | use                                                                                                                            | eas                               | <br>\$   |             | ty.                                         | чн.                                                          | Ξ   | HHP                                                          | GAS                                                          |
|   | ırd;               | (f1                       | ion                                                                                                                 | i B                                  | Sm;                                  |                                         |                     | ce              |                            |      | CAO          | ģ    | GOSSARD F.  | CZD          | TREMBLAY | F, Hamet     | WPI; 98-077171/07. | ٠.<br>۾         | rel                                         | ed 4                                     | 25.2        | ai mi                                                               | )<br>je                                                             | ü       | ıgai                                                               | ğ                                                  | g g                                                                                                                            | dis                               | 224 AA;  |             | Best Local Similarity<br>Matches 178; Conse | APYI                                                         | Ξ   | rPYI                                                         | VEQI                                                         |
|   | ande               | 86                        | tens                                                                                                                | lai.                                 | oidi                                 | ttus                                    |                     | erer            | ,<br>,                     | 97.  | 97;          | 96;  | AME<br>TAKE | WA           | REM      | H,           | 771                | 188             | i c                                         | 20.5                                     | Page        | Pe                                                                  | geī                                                                 | ssic    | άγ                                                                 | and<br>1                                           | 117                                                                                                                            | ory                               | N        |             | Simi<br>178;                                | GAA                                                          | Ξ   | GAA                                                          | REA                                                          |
|   | st.                | -19                       | per                                                                                                                 | e11                                  | hyr                                  | cancer; inital<br>Rattus rattus         |                     | Misc_difference | C K - 70 90 4 7 90W        | -19  | 23-JUN-1997; | 61 : |             |              |          | EI<br>O      | 0-8                | N-PSDB; V18890. | ens                                         | rs<br>S                                  | 2           | is.                                                                 | ted                                                                 | pre     | oqi                                                                | enn                                                | hvr                                                                                                                            | mat                               | e<br>S   | ch<br>C     | 11 S                                        | SAL                                                          | =   | ISAV                                                         | KDC                                                          |
|   | T 1<br>W37723      | Ę                         | Hy                                                                                                                  | rac                                  | ert                                  | Cancer;<br>Rattus r                     |                     | ű               | 7 4 0                      | DEC  | ND.          | 5    | (GOSS/)     | (LEWA/)      | (TREM/)  | Gossard      | ъ<br>.:            | SDB             | Sert                                        | anc                                      | i E         | 5                                                                   | Jula                                                                | ě       | ant                                                                | 5                                                  | SCLI                                                                                                                           | lam                               | sequence | Mat         | S S                                         | -                                                            |     | ~<br>H                                                       | 61 6                                                         |
|   | W37                | 6                         | Rat                                                                                                                 | ext.                                 | hyr                                  | Rate                                    | Key                 | Mis             | Ç                          | 31   | 23           | 21   | 5 2         | įĒ           | E        | Š            | WPJ                | ż               | HYE                                         | d, c                                     | ם מ         | 뎙                                                                   | re                                                                  | Its     | P.                                                                 | e i                                                | Spe                                                                                                                            | 1                                 | Š        | Query Match | Best Lo<br>Matches                          |                                                              |     |                                                              | ·                                                            |
|   | RESULT<br>ID W     | 25                        | DE<br>KE                                                                                                            | KW                                   | K.                                   | ž O                                     | 표                   | 댎               | FT                         |      | PF           | PR.  | 4 4<br>4 4  | ( <u>4</u>   | PA       | ΡΙ           | œ                  | DR              | 탪                                           | - E                                      | ı ço        | ن ا                                                                 | ខ                                                                   | ပ္ပ     | ប្តូច                                                              | 2 6                                                | 38                                                                                                                             | 888                               | ġ.       | å           | Be                                          | q                                                            | ! . | ŏ                                                            | g                                                            |
|   | жна                | Ω                         | CIF                                                                                                                 | <b>×</b>                             | × 1                                  | 40                                      | 14                  | 124             | 14 6                       | 4 04 | щ            | щ    | ъ, D        | , д.         | 124      | 14           | ы                  | Ц               | L14 E                                       | <b>14</b> D                              | <b>.</b> D. | O                                                                   | J                                                                   | J       | 0 (                                                                | ) (                                                | <i>-</i>                                                                                                                       |                                   | 0,3      |             |                                             |                                                              | l)  | •                                                            | ч                                                            |

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New tumorigenesis associated protein and related nucleic acid, vectors, transformed cells - antibodies, agonists and antagonists, vectors, transformed cells - antibodies, agonists and antagonists, for diagnosis, treatment and prevention of abnormal cellular differentiation, particularly cancers and inflammation.

This is the amino acid sequence of the human tumourigenesis associated protein (HTAP), used in the method of the invention. HTAP, is involved with cell proliferation and inflammation. It can be used to stimulate cell proliferation and inflammation. It can be used to stimulate cell proliferation of tumours or infections, or to treat genetic defects). Antagonists of HTAP are used to treat or prevent a wide range of cancers (adenocazcinoma, melanoma, sarcoma, lymphoma, leukaemia etc.), also inflammation where associated with infection or anthritis). HTAP is also used to raise antibodies are used as for diagnosis or monitoring of HTAP-related diseases (in usual immonoassays), in competifitie drug screens and to isolate HTAP from immunoassays), in competifitie drug screens and to isolate HTAP from standard amplification or hybridisation tests to diagnose HTAP-related diseases; to identify related sequences; for genomic mapping and for screening for specific inhibitors.
 ä
 Human secreted protein fragment encoded from gene 16.
Human; secreted protein; treatment; prevention; protein therapy; AIDS;
 DLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQL 180
LED-CKFDRERI-ELFCTEYQNNKNSLEILLGSIGRSLPHITDVSWRLEYQIKTNQLHRM 144
 Gaps
 04-DEC-1998 (first entry)
Amino acid sequence of the human tumourigenesis associated protein.
Human: tumourigenesis associated protein; HTAP; transplantation;
tumour; Antagonist; cancer; inflammation; immunological disease;
antibody; probe; primer; PCR; amplification; hybridisation;
inhibition.
 Score 122; DB 1; Length 195;
Pred. No. 6.45e-01;
35; Mismatches 38; Indels
 145 YRPAYLVTLSVQNTDSPSYP-EISFSCSMEQLQDLVG-KLKDASKSLER 191
 181 KLTDGSAHRFEVPIAKFQELRYSVALVLKEMAELEKKCERKLQD
 RESULT 2
ID W71684 standard; Protein; 195 AA.
 r 3
Y07867 standard; Protein; 196 AA.
 Query Match 7.6%;
Best Local Similarity 24.8%;
Matches 27; Conservative
 20-MAR-1998; U06066.
20-MAR-1997; US-822260.
(INCY-) INCYTE PHARM INC.
GOLL SK, HILLMan JL;
WPI: 98-521224/44.
N-PSDB; V58281
 06-JUL-1999 (first entry)
 Homo sapiens.
WO9841635-A1.
 24-SEP-1998
 W71684;
 121
 181
 87
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proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal efficiencies, blood disorders, leukemiss, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lumphomas; inflammation, allergies, Alzheimer's and cognitive disorders, pulmonary disorders, transplant rejection, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseative/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in X37451-X37552.

Sequence 196 AA;
gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia; cognitive disorder; prostate disease; skeletai; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoprosis; arthritis; malignancy; digestive; endocrine; infection.
 ŝ
 87 LED-CKFDRERI-ELFCTEYQNNKNSLEILLGSIGRSLPHITDVSWRLEYQIKTNQLHRM 144
 113 LQELC-IPQDLVGDLASVVFGSQRPLLDSVAQQQGAWLPHVADFRWRVDVAISTSALARS 171
 New isolated human genes and the secreted polypeptides they encode Claim 1b; Page 285-286; 368pp; English. This invention describes novel isolated human genes and the secreted
 Gaps
 <u>ن</u>
 cancer;
 26-APR-1999 (first entry)
Human Zneul partial polypeptide.
Zneu-1; neuro-growth factor-like protein; human; breast cancer;
glikoblastoma; pituitary adenoma; Alzheimer's disease; therapy;
nerve regeneration; haematopolesis; fertility; contraception;
antibody.
 Length 196,
 145 YRPAYLVTLSVQNTDSPSYP-EISFSCSMEQLQDLVG-KLKDASKSLER 193
 Score 122; DB 1; Length 196
Pred. No. 6.45e-01;
35; Mismatches 38; Indels
 02-0CT-1997; US-060884.
02-0CT-1997; US-060833.
02-0CT-1997; US-060836.
02-0CT-1997; US-060836.
02-0CT-1997; US-060837.
02-0CT-1997; US-060843.
02-0CT-1997; US-060866.
02-0CT-1997; US-060866.
02-0CT-1997; US-060866.
02-0CT-1997; US-06087.
02-0CT-1997; US-06087.
03-0CT-1997; US-06087.
03-0CT-1997; US-060886.
03-0CT-1997; US-06087.
03-0CT-1997; US-06087.
03-0CT-1997; US-06087.
03-0CT-1997; US-06087.
03-0CT-1997; US-06087.
03-0CT-1997; US-06087.
03-0CT-1997; US-0CT-1997;
 Ä
 W88390 standard; Protein; 169
 Query Match
Best Local Similarity 24.8%;
 N-PSDB; X37466.
 Homo sapiens
 Homo sapiens
 15-APR-1999
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178 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQ-QL 228
 Domain
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 4;
 New manumalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells

Zlaim 6; Page 57-58; 70pp; English.

This claimed polypeptide comprises amino acid residues 105-273 of the human Zneul mature protein (see W88382), i.e. the 2 epidermal growth factor-like domains (see also W88384-85) and the second HSMHC3W5A homology domain of Zneul. Zneul is a new neuro-growth factor-like protein that can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. Zneul may also play a role in breast cancer, glioblastomas, and plutitary adenomas. Zneul can be used to treat Alzheimer's disease, cancer, to repopulate blood cells cancer, glioblastomas, and plutitary adenomas. Zneul can be used to treat Alzheimer's disease, cancer, to repopulate blood cells cancer menotherapy, to stimulate myofilroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed cancer inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed of Zneul and epitope-bearing portions of Zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.
 Gaps
 fertility and contraception, or to regenerate nerves. Claimed
Eneul polypeptides (see also W88382-97), including specific domains
 This claimed polypeptide comprises amino acid residues 1-85 and first HSMHC3W5a homology domain fused to the second HSMHC3W5a homology domain fused new neuro-growth factor-like protein that can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. Zneul may also play a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul can be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in
 e.g. treat Alzheimer's
 W88391;
26-APR-1999 (first entry)
Human Zneul partial polypeptide.
Aneu-1; neuro-growth factor-like protein; human; breast cancer;
glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
nerve regeneration; haematopoiesis; fertility; contraception;
 4;
 93 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQ-QL 143
 Score 116; DB 1; Length 169;
Pred. No. 1.72e+00;
9; Mismatches 16; Indels
 (ZYMO) ZYMOGENETICS INC.
Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO,
Whitmore TE;
 (ZYMO) ZYMOGENETICS INC.
Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO,
Whitmore TE;
 New mammalian Zneul polypeptides - used to, e. disease, cancer and to repopulate blood cells Claim 6; Page 58; 70pp; English.
 W88391 standard; Protein; 181 AA.
 Query Match
Best Local Similarity 44.2%;
Matches 23; Conservative
 23-DEC-1998.
18-JUN-1998; U12763.
18-JUN-1997; US-878322.
18-JUN-1997; US-050143.
 23-DEC-1998.
18-JUN-1998; U12763.
18-JUN-1997; US-878322.
18-JUN-1997; US-050143.
 WPI; 99-095324/08.
 WPI; 99-095324/08.
 Homo sapiens.
WO9857983-A2.
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Wew manumalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells

Glaim & Page 48.49; 70pp; English.

This polypeptide comprises human Zneul mature polypeptide. Zneul closest human homologue is HSMHC3M5A, a gene in the HLA class III region, which is contained in a cosmid which contains Notch 4.

To region, which is contained in a cosmid which contains Notch 4.

Cancul is also homologue to Notch 4 in its EGF-like domains and may be involved in EGF receptor pathways. Zneul is widely expressed in adult tissues, with high expression in heart, placenta, spleen, testis, thyroid, spinal cord and lymph node. Zneul can be used as growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. In may law a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul may also be used to treat Alzheimer's disease, adenomas. Zneul may also be used to treat Alzheimer's disease, and in the placenta, in fertility and contraception, or to myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to including specific domains of Zneul and epitope-bearing portions of cancer. Cancer cance
 Gaps
 Gaps
 /note= "hydrophilic domain (HSM1), homologous to
an HSMHG3W5A domain "
 26-APR-1999 (first entry)
Human neuro-growth factor-like protein Zneul mature polypeptide.
Zneu-1; neuro-growth factor-like protein; human; breast cancer;
glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
 7.000 - Processor 3.000 - 1.00
 /note= "domain HSM2 homologous to an HSMHC3W5A
 epidermal growth factor-like domain 1"
 4;
 .,
 105 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQ-QL 155
 nerve regeneration; haematopolesis; fertility; contraception; antibody.
of Zneul and epitope-bearing portions of Zneul, can be used raise specific antibodies for use e.g. in diagnostic assays. Sequence 181 AA;
 Score 116; DB 1; Length 254;
Pred. No. 1.72e+00;
 Score 116; DB 1; Length 181;
Pred. No. 1.72e+00;
 Indels
 9; Mismatches 16; Indels
 9; Mismatches 16;
 (ZIMO) ZIMOGENETICS INC.
Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO,
MILHGROTE TE:
WPI: 99-095324/08.
 Location/Qualifiers
 r 6
W88382 standard; Protein; 254 AA.
 Query Match 7.2%;
Best Local Similarity 44.2%;
Matches 23; Conservative
 Query Match
Best Local Similarity 44.2%;
Matches 23; Conservative
 .116
 23-DEC-1998.
18-JUN-1998; U12763.
18-JUN-1997; US-878322.
18-JUN-1997; US-050143.
 Homo sapiens.
 Sequence
 W88382;
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standard; Protein; 800 AA.

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Matches
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 New manumalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells

I disease, cancer and to repopulate blood cells

Claim 6; Page 47-48; 70pp; English.

This polypeptide comprises human Zneul, a new neuro-growth factor-

I like protein. Its amino acid sequence was deduced from the nucleotide sequence (see V84341) of a CDNA clone isolated from a commit on the HLA class III region, which is contained in a cosmid which contains Notch 4. Zneul is also homologue is HSMHC3W5A, a gene in the HLA class III region, which is contained in a cosmid which contains Notch 4. Zneul is also homologues to Notch 4 in its GGF-like domains and may be involved in EGF receptor pathways.

EGF-Like domains and may be involved in EGF receptor pathways.

Eneul is widely expressed in adult tissues, with high expression in heart, placenta, spleen, testis, thyroid, splinal cord and lymph nodes. Zneul polypeptide can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. It may also play a role in breast cancer, cliobiastomas, and pituitary adenomas. Zneul may be used to treat chemotherapy, to stimulate myofibroblast prolliferation, stimulate contractors and envise. Claimed Zneul into to respond to the placenta, in fertility and contraction.
 can be used to raise
 /note= "hydrophilic domain (HSM1), homologous to
an HSMHC3W5A domain "
 contraception, or to regenerate nerves. Claimed zneul polypeptides (see also W88382-97), including specific domains of zneul and epitope-bearing portions of zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.
 26-APR-1999 (first entry)
Human neuro-growth factor-like protein Zneul.
Zneu-1; neuro-growth factor-like protein; human; breast cancer;
glloblastoma; pituitary adenoma; Alzheimer's disease; therapy;
nerve regeneration; haematopolesis; fertility; contraception;
antibody.
 "epidermal growth factor-like domain 1"
 "epidermal growth factor-like domain 2"
 /note- "domain HSM2 homologous to an HSMHC3W5A
65 RDGVQRLGVSANLPEEQLGALLAGMHTLLQQAL-R-LP-PTSLKPDTFRDQL 113
 Score 116; DB 1; Length 273;
Pred. No. 1.72e+00;
9; Mismatches 16; Indels
 16; Indels
 /note= "putative signal peptide"
 18-JUN-1997; US-878322.
18-JUN-1997; US-050143.
18-JUMDerg H, Jelinek LJ, Lehner JM, Sheppard PO,
 /note= "mature protein"
 Location/Qualifiers
 W88381 standard; Protein; 273 AA.
 domain"
 e,
/note= "ep[†]
178.
 Query Match
Best Local Similarity 44.2%;
Matches 23; Conservative
 .135
 104
 /note=
136. .1
 105.
 .8-JUN-1998; U12763
 Whitmore TE;
WPI; 99-095324/08.
 N-PSDB; V84341.
 Homo sapiens.
 W09857983-A2.
 Sequence
 Peptide
 Protein
 Domain
 Domain
 Domain
 Domain
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NEW MARKET PROPERTY P

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Eckner R, Ewen M, Livingston D;
WPI; 95-373813/48.
Nucleic acid encoding human p300 that associates with adenovirus ElA - and related vectors, host cells and screening assays, also diagnosis of cancerous and pre:cancerous tissue by detection of
 Nucleic acid encoding human p300 that associates with adenovirus ElA - and related vectors, host cells and screening assays, also dlagnosis of cancerous and pre:cancerous tissue by detection of
 Gaps
 Disclosure: Page 61-78; 126pp; English.

Transcription factor p300 was isolated from human 293 cells and used to generate polyclonal antisera in mice. These were used to screen 293 cDNA libraries to isolate clones conty. overlapping inserts, which were assembled to obtain a full-length cDNA sequence (T02792)
 /label-C/H-rich_region_1
/note= "cysteine/histidine-rich region containing
2 putative zinc finger motifs"
1070. 1134
 mutant p300
Claim 17: Page 72-78: 126pp; English.
A fusion protein comprising glutathione-S-transferase and amino acids 1572-2371 (R84883) of human transcription factor p300 (full sequence given in R84882) was used to produce an anti-p300 monoclonal antibody (MAb) useful in identifying p300 binding
 AB4882 standard; Protein; 2414 AA.
R84882 standard; Protein; 2414 AA.
01-FEB-1996 (first entry)
Transcription factor p300.
Transcription factor; p300; adenovirus; early region IA; ElA; cancer; diagnosis.
 ;
;
 566 QAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQ-MNMNHNTM-PSQFRDILR 613
 Length 800
01-FEB-1996 (first entry)
Transcription factor p300 C-terminal (1572-2371) region.
Transcription factor; p300; adenovirus; early region 1A; cancer; diagnosis; monoclonal antibody.
 Score 110; DB 1; Length 800
Pred. No. 4.50e+00;
13; Mismatches 18; Indels
 proteins and for characterizing p300 in immunoassays.
 11. .17
/label= Nuclear_location_signal
 1162. .1461
/label- C/H-rich_region_2
1622. .1821
/label- C/H-rich_region_3
 14-APR-1994; US-227536.
(DAND) DANA FARBER CANCER INST INC.
ECKNER R, EWEN M, LIVINGSTON D;
WWPI; 95-373813/48.
N-PSDB; T02792.
 070. .1134
label- Bromodomain
 Location/Qualifiers
 13-APR-1995; U04682.
14-APR-1994; US-227536.
(DAND) DANA FARBER CANCER INST II
ECKNER R, EWEN M, LIVINGSTON D;
 Match 6.9%;
Local Similarity 34.0%;
 17; Conservative
 .421
 26-OCT-1995.
13-APR-1995; U04682.
 800 AA;
 26-OCT-1995.
 WO9528499-A1.
 Sequence
 Query Match
 peptide
 region
 doma1n
 region
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Gaps

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197 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQ-QL 247

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Sugar biosynthesis enzyme EryCII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W99387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated p300/CBP-associated factor, P/CAF - used to develop products for modulating transcription, e.g. for treating HIV products for modulating transcription, e.g. for treating HIV products for modulate or for promoting muscle differentiation or access or for promoting muscle differentiation or particular page 76-81; 107pp; English.

This polypeptide sequence comprises p300, a global transcriptional coactivator that is involved in the regulation of various DNA-binding transcriptional factors. The invention relates to a novel human p300/CBP associated cofactor, P/CAF (see W40052), that modulates transcription through binding to p300 and CBP (see W40058). The region (see W40055) of p300 that binds to P/CAF is claimed. The Invention provides methods of screening for compounds that inhibit or stimulate the transcription modulating and histone acetyltransferase activity of P/CAF and p300/CBP.

Inhibitors can be used e.g. to inhibit HIV TAT-mediated transcription in the treatment of HIV infection. Stimulators can be used e.g. to activate tumour suppressor p53 in the treatment of cancer or to activate the muscle differentiation factor MyoD to promote muscle differentiation. The products can also be used to inhibit the cell cycle progression inducing effect of an oncoprotein which binds p300/CBP in a subject. Also provided is contacting the sample with the P/CAF binding region of p300 and determining the amount of P/CAF in a sample by sequence 2414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                          Gaps
encoding a protein (R84882) of predicted mol.wt. 264.236 kDa. 3300 may be produced in host cells (pref. mammalian) and used to raise monoclonal antibodies or to screen cpds. for the ability to modulate p300-dependent transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-1998 (first entry)
Cellular transcriptional factor p300.
Cellular transcriptional factor; p300; human; p300; p/CAF;
transcription; histone acetyltransferase; HIV; infection; cancer;
therapy; muscle differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2137 QAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQ-MNMNHNTM-PSQFRDILR 2184
                                                                                                                                                                                                                                 2137 QAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQ-MNMNHNTM-PSQFRDILR 2184
                                                                                                                                       Score 110; DB 1; Length 2414;
Pred. No. 4.50e+00;
13; Mismatches 18; Indels 2
                                                                                                                                                                                                                                                              Score 110; DB 1; Length 2414;
Pred. No. 4.50e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1763. .1966
/note- "P/CAF binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-1997; U12877.
23-JUL-1996; US-022273.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 T 10
W40057 standard; Protein; 2414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.0%;
Matches 17; Conservative
                                                                                                                                       / Match 6.9%;
Local Similarity 34.0%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH
Howard BH, Nakatanl Y;
WPI; 98-120777/11.
N-PSDB; V10092.
                                                                                            2414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9803652-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-1998
                                                                                              Sequence
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                               W40057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                   RESULT
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LT 11 W19734 standard; Protein; 360; W19734; 18-SEP-1997 (first entry)

RESULT ID W1' AC W1 DT 18

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New nucleic acid sequences encoding enzymes involved in macrolide bosynthesis. - useful for producting hybrid secondary metabolites, particularly erythromycin analogues claim 6; Fig 2; 221pp; French.
This sequence represents the dTDP-4-keto-L-6-deoxyhexose-3,4-isomerase enzyme encoded by the eryCII gene from the eryG-eryAIII gene cluster from the Gram-positive bacterium Saccharopolyspora erythraea. This gene cluster encodes enzymes involved in the production of the macrolide antibiotic erythromycin as a secondary metabolite. The erythromycin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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S.erythraea dTDP-4-keto-L-6-deoxyhexose-3,4-isomerase.
Gene cluster, bacterium; enzyme; macrolide; antibiotic; erythromycin; secondary metabolite; eryBlI; eryCIII; eryCIII; hybridisation; probe; glycosylation; macrolactone; oleandomycin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 QGEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 MTAVLGAAGVLR--GAAWDARVS-LDAQLSPQQLAVTEAAVAALPADPALRAL-FAGAEM 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 TANTVVDAVLAVSAEPGLAE-RIADDPAAAQRIVAEVLRLHPA-LHLER-RTATAEVRLG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSAVGAATPYLHHPGDSHSGRVSFLGAQLPPE-VAAMARLLGDLDRSTFRKLLKFVVSSL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosylation
Disclosure: Fig 4A; 85pp; English.
Disclosure: Fig 4A; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534; 919534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes involved in sugar biosynthesis and attachment - used t
generate polyketide antimicrobials etc. with altered pattern of
    D-desosamine; antimicrobial;
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Polyketide; glycosylation; eryCII; D-desosamine; antimicro antibiotic; antifungal; fungicide; anticancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 107; DB 1; Length 360
Pred. No. 7.24e+00;
36; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HMRI ) HOECHST MARION ROUSSEL.
COrtes J, Gaisser S, Leadlay P, Michel JM, Raynal MC, Salah-Bey K, Fromentin C, Mendez C, Salas JA;
                                                                                                                                                                                                                                                                                                                                                                       Summers RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r 12
W99387 standard; Protein; 361 AA.
                                                                                                                                                                                                                                                                                                                                                               Donadio S, Katz L, Staver MJ,
WPI; 97-351066/32.
N-PSDB; T72684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharopolyspora erythraea.
WO9905283-A2.
                                                                                                                      Saccharopolyspora erythraea.
WO9723630-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f. Match
Local Similarity 25.2%;
les 33; Conservative
                                                                                                                                                                                              03-JUL-1997.
23-DEC-1996; U20238.
21-DEC-1995; US-576626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1998; F01593.
12-JUN-1998; FR-007411.
25-JUL-1997; FR-009458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 EHVIGEGEEVV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ODLVGDLASVV 130
                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 99-142938/12.
                                                                                anthelmintic.
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frames (ORF). The genes are used to produce hybrid secondary metabolites in S.erythraea, i.e. erythromycin analogues which may have improved properties or as hybridisation probes for isolating homologous genes involved in glycosylation of macrolactones in macrolide-producing strains (specifically oleandomycin-producing strains of Streptomyces
                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
;
                                                                                                                                           151 MTAVLGAAGVLR--GAAWDARVS-LDAQLSPQQLAVTEAAVAALPADPALRAL-FAGAEM 206
                                                                                                                                                                                                    60 QEEDCRDGVQRLGVSANLPEEQLGALLAGMHTLLQQALRLPPTSLKPDTFRDQLQELCIP 119
                                                                                                                                                                                      207 TANTVVDAVLAVSAEPGLAE-RIADDPAAAQRTVAEVLRLHPA-LHLER-RTATAEVRLG 263
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 LSTEEKAAAIDRL--RASLPEDQQESVLPQLQSELQQQTAALQAAGAGPEAIRQMRQQL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R77317 represents a mew protein-activated lipase. The protein is produced as a fusion protein with glutathionine transferase. The protein has an amino acid sequence of 339 residues and a molecular weight of 39 kD. The method used to produce the new protein yields active lipase of very high purity without using any complex purification process such as chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion
                                                                                                                                                                                                                                                                                                                                                                                                   (TOYM ) TOYOBO KK.
WPI: 95-227395/30.
N-PSDB: 091399/30.
A new protein for activating lipase - may be produced as a fusic protein with glutathione transferase, used in the production of
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                                                                                                   Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 339;
                                                                                                 Score 107; DB 1; Length 361
Pred. No. 7.24e+00;
36; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106; DB 1; Length 339
Pred. No. 8.48e+00;
21; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                 07-FEB-1996 (first entry)
Protein activated lipase B.
Lipase B; activate; glutathionine transferase.
307135971-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-1999 (first entry)
Human VRRP-1 (VR2) capsaicin receptor.
                                                                                                                                                                                                                                                                                                Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 6-7; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. 14
W99798 standard; Protein; 727 AA.
                                                                                                                                                                                                                                                                                    T 13
R77317 standard; Protein; 339
                                                                                                 6.7%;
ilarity 25.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1995.
05-JUL-1993; 165561.
05-JUL-1993; JP-165561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U17466.
US-072151.
                                                                                                                                                                                                                                                    120 ODLVGDLASVV 130
                                                                                                                                                                                                                               264 EHVIGEGEEVV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                           Local Similarity
nes 33; Conser
                                                                              361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-1999.
20-AUG-1998; U
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WO9909140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W99798;
16-JUN-1999
                                                                              Sequence
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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Matches
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Claim 4: Page 86-88: 99pp; English.

Claim 4: Page 86-88: 99pp; English.

The present sequence is an isolated capaaicin receptor polypeptide

(I). Capsalcin polypeptides are useful for identifying binding compounds

which affect cellular responses. Preferably this is for identifying a

compound that binds (I) and affects a cellular response associated with

capsalcin biological activity (e.g. intracellular calcium flux). The

polypeptides and host cells are useful for detecting a vanilloid

compound (an essential structural component of capsalcin) from natural

products by detecting an alteration of intracellular response associated

with capsalcin receptor activity, preferably an alteration of

intracellular calcium levels, and are useful for screening for compounds

for use in analgesics. Capsalcin receptor polypeptides and antibodies

are useful for diagnosis and treatment of human diseases and painful

syndromes. The transgenic mammals can be used to screen for capsalcin

receptor antagonists and agonists. Prior art methods for iscreening or

characterising new capsalcin receptor-binding compounds relied on assays

polypeptides provide a more sensitive screen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 ASLQAIDSQGNTVLHALVMISDNSAENI-ALVTSMYDGLLQAGARLCPT-VQLEDIRN-L 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increasing lipase prodn. In Pseudomonas species - by cloning a lipase gene and a lipase modulator gene into a homologous Pseudomonas species benedictured in the lipase gene from Pseudomonas pseudoalcaligenes MI was cloned in E. coli as in EP-334462. The DNA sequence of insert Pvul/EcoRI contains two open reading frames, one encoding the lipase gene, the other encoding a putative lipase modulator gene which increases the lipase productivity in a homologous host cell. The lipase obtd. is used for hydrolysing lipids in e.g. fats and oil processing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas; cloning; lipase gene; lipase modulator gene; lipids; oils; fats; detergents; diagnostic reagents.
Pseudimonas pseudoalcaligenes.
WO9402617-A.
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                                                                                                                                       New capsaicin receptor polypeptide - useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106; DB 1; Length 727
Pred. No. 8.48e+00;
24; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 104; DB 1; Length 344
Pred. No. 1.16e+01;
38; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detergents or diagnostic reagents See also R47212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R47213 standard; Protein; 344 AA
20-AUG-1997; US-915461.
(RRGC) DNIV CALIFORNIA.
Brake A, Caterina M, Julius DJ;
WPI: 99-181023/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 QDL-TPLKLAAKEGKIXIFXRH 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 OELCIPODLVGDLASV-VFGSQ 134
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Best Local Similarity 29.3%;
Matches 24; Conservative
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Best Local Similarity 21.7%;
Matches 26; Conservative
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(KONN ) GIST-BROCADES NV.
COX MMJ, Gerritse G, Qu
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23-JUL-1993; E01995
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N-PSDB; Q56106.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri May 12 10:24:14 2000; MasPar time 81.94 Seconds 189.543 Million cell updates/sec Tabular output not generated. MPsrch_pp Run on:

>US-09-223-796-2 (1-224) from US09223796.pep 1552 1 MSALGAAAPYLHHPADSHSG......ALVLKEMAELEKKCERKLQD 224 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 segs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus sptremb112

Mean 45.804; Variance 101.760; scale 0.450 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length DB	g .	ΩI	Description	Pred. No.
1	124	8.0	195 1	-	063829	BUP-5'OF BMI-1 PROVIRA	4.75e-03
7	121	7.8	491	~	P73944	HYPOTHETICAL 55.6 KD P	1.15e-02
e	119	7.7	202	4	Q9Y6G5	PID002.	2.05e-02
4	120	7.7	649	4	043642	HEAT SHOCK PROTEIN 75.	1.54e-02
Ŋ	118	7.6	512 1	9	Q9ZW95	F5A8.3 PROTEIN.	2.74e-02
w	118	7.6	949	ß	Q27512	NEX-2 PROTEIN.	2.74e-02
7	110	7.1	206	~	P72747	HYPOTHETICAL 79.8 KD P	2.64e-01
80	107	6.9	470	Ŋ	062159	F13G11.1 PROTEIN.	6.02e-01
δ	107	6.9	913	Ŋ	P90742	CODED FOR BY C. ELEGAN	6.02e-01
10	105	6.8	279	7	092553	FLAGELLIN.	1.03e+00
11	104	6.7	226 1	7	098184	MC013L.	1.35e+00
12	104	6.7	228	_	Q9YBI8	228AA LONG HYPOTHETICA	1.35e+00
. 13	104	6.7	302	6	037840	P2 J HOMOLOG.	1.35e+00
14	104	6.7	382	7	Q9X7Y2	PROBABLE ACYL-COA DEHY	1.35e+00
15		6.7	603 1	_	070211	INSULIN-LIKE GROWTH FA	1.35e+00
16	104	6.7	1116	~	P73507	DNA POLYMERASE III SUB	1.35e+00
17		6.7	4845 1	디	088738	UBIQUITIN-CONJUGATING	1.35e+00
18		9.9	164	~	087525	GALACTOSE-1-PHOSPHATE	2.30e+00
19		9.9	451	~	P72863	HYPOTHETICAL 49.7 KD P	2.30e+00
20	103	9.9	555	7	092924	FRUCIOSE-6-P PHOSPHOIR	1.77e+00

1.77e+00 3.90e+00 5.05e+00 5.05e+00 5.05e+00 5.05e+00 5.05e+00 6.54e+00 6.54e+00 6.54e+00 6.54e+00 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01
SPINDLE POLE BODY PROT L.ZIP+NBS+LRR. PUTATIVE TRANSCRIPTION PROLIFERATING CELL NUC FINBRIAL PROTEIN. 362AA LONG HYPOTHETICA UDD-N-ACETYLGLUGOSAMIN NUCLEOPORIN. SERINE-THREONINE PROTE BLACKJACK. 30S RIBOSOWAL PROTEIN GALR-LACI HOMOLOG. HYPOTHETICAL 40.9 KD P PTXR. TRANSCRIPTIONAL ACTIVA HYPOTHETICAL 40.9 KD P ELONGATION FACTOR EF-G RECEPTOR-LIKE PROTEIN C457.6 PROTEIN. F5566.2 PROTEIN. F5566.3 PROTEIN. F5566.3 PROTEIN. F5566.3 PROTEIN.
043632 092QT7 092QT7 09W5HD3 09W720 047220 0094324 0094324 0094324 0026471 0094324 0020333 0020333 0020333 0020333 0020233 0020233 0020233 0020233 0020233 0020233 0020233 0020233 0020234 0020234 0020234 0020234 0020234 0020234 0020234 0020234 0020234 0020234
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ALIGNMENTS

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PRT;

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                                                                    MEDLINE; 97061201.

KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                           121 RELNRN-YTKALQLLRRVSEQSRNLRQEVANLSAERAQLNEQK-DSLLAESSELQSQVKL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 LETISFILEGAV-YH--NVKPAALQQQLENIHLRQDKAEAFVN-TWSSMGQETVEKFRQR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAGTHILLQQALRLPPASLKPDAFQEELQELGIPQDLIGDLASLAFGSQ-RPLLDSVAQQ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 : 1 : 1 : 1 : 1 : 1 : 30 SPEVTAVAQLLKDLORSTERKLKLVGALHGK-DCR--EAVEQ-LGASANLSEERLAVL 85
                                                                                                                                                                                                                                                                                                          12 SPSMKKAVSLINAIDTGRFPRLLTRILQKLHLKAESSFSEEEEKLQAAFSLEKQDLHLV 71
                                                                                                                                                       "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; EMBL, D90911, BAA18010.1; -...
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                       179 RDQELSKRQERIAQQEKVLARQREQVQSLEKRFASLEAQRQQLQAEINQRDTKIDQL 235
                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A.
TISSUE-PITUITARY TUMOR;
FU G., HUANG Q., SONG H., PENG J., ZHANG Q., MAO M., DAI M., MAO ZHOU J., CHEN Z., CHEN J.;
HUMIAN PIDDOL2 MRNA, complete cds.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078857; AAD44489.1;
SEQUENCE 202 AA; 22966 MW; 51317189 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 119; DB 4; Length 202;
Pred. No. 2.05e-02;
53; Mismatches 72; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 ILAP-CKLETVGWQLNLQMAHSAQAKLKSPQAVLQLGVNNEDSKSLEKVLVEF 179
                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                   Length 491;
                                                                                                                                                                                                                                               Score 121; DB 2; Length 491
Pred. No. 1.15e-02;
36; Mismatches 47; Indels
                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          55645 MW; 6EFDFCFA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                          202
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                                                                                                                                                                                                                                               Query Match 7.8%;
Best Local Similarity 23.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.7%;
Best Local Similarity 22.0%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                          Submitted (JUN-1996)
                                                                                                                                                                                                                          491 AA;
         SEQUENCE FROM N.A. STRAIN-PCC6803;
                                                                SEQUENCE FROM N.A.
                                 TABATA S.
                                                                                                                                                                                                                           SEQUENCE
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Q9Y6G5
Q9Y6G5;
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MEDLINE; 96347537.
CHEN C.F., CHEN Y., DAI K., CHEN P.L., RILEY D.J., LEE W.H.;
"A new member of the hsp90 family of molecular chaperones interacts
with the retinoblastoma protein during mitosis and after heat shock.";
Mol. Cell. Biol. 16:4691-4699(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 KKLLDIVARSLYS-E-KEVFIRELISNASDALEKLRHKLVSDGQALPEMEIHLQTNAEKG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 WTLMLLAHNPTWQDNVRDEVRQVCGQDGVPSVEQLSSL-TSLNKVINESLRLYPPATLLP 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. COLUMBIA;
FEDERSTIEL N.A., PALM C.J., CONWAY A.B., KURIZ D.B., CONWAY A.R.,
AU M., ARAUJO R., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y.,
OJI O., OSBORNE B.I., SHINN P., SUN H., TORIUMI M., VYSOTSKAIA V.S.
YU G., ECKER J., THEOLOGIS A., DAVIS R.W.;
SUDMILTED (JAN-1999) to the EWBL/GenBank/DDBJ databases.
EMBL; ACO04146; AADIOSSI.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 649;
                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A. CHEN P.L., RILEY D.J., LEE W. CHEN C.F., CHEN J.D. LEE W. SUDMITTED (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF043254; AAC02679.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 4; Length 649
Pred. No. 1.54e-02;
40; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 118; DB 10; Length 51
Pred. No. 2.74e-02;
20; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 TITIQD-TGIGMTQEELVSNLGTIARSGSKAFLDALQNQAEAS 142
                        Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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    Created)
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PFAM; PF00183; HSP90; 2.
PRINTS; PR00775; HEATSHOCK90.
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Local Similarity 32.1%;
nes 25; Conservative
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Local Similarity 22.3%;
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                     N-1998 (TrEMBLrel.
N-1999 (TrEMBLrel.
SHOCK PROTEIN 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                 Homo sapiens (Human).
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01-JUN-1998
01-JUN-1998
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat shock.
SEQUENCE
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MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., KERSHAW J., LISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MONTHANAY J., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SYALLON N., SMITH A., SONNHAAMER E., STADEN R.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATSON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.;

2. 2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 STDFIQKSEDLK-DEEKVALERIVEQKLAESAKNEKDIAWNVIVVANSYVAKSLRPVIN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 PQDLIGDLASLAFGSQRPLLDSVAQQQ-GSSLPHVSYFRWRVDVAISTSAQSRSLQPSVL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 C-ELVKESRSHEMLSEEQLATLYDCATTSTRLPNDFADDQEDLKNIIRYGELFKACHAIN 117
                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
-!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION IN INVOLVED IN EXOCYTOSIS.
-!- SIMILARITY: TO OTHER PROTEINS OF THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 118; DB 5; Length 676;
Pred. No. 2.74e-02;
31; Mismatches 67; Indels
                                                                                                                                                                                                                           Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 79.8 KD PROFEIN.
Synechocystis Sp. (Strain PCC 6803).
Bacteria, Cyanobacteria, Chrococcales; Synechocystis.
                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01223; ANNEXIN; 1.
PFAM; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
SEQUENCE 676 AA; 74969 WW; 00E36C79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 AA
                                                                       676 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
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                                                                                                Created)
                                                                        PRT;
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178 MQLKLTDGSAHRFEVPIAKFQELR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 IQMPTVGGDIN-FEFDIDSFAQFR 199
                                                                                                01,
12,
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Best Local Similarity 25.7%;
Matches 37; Conservative
  392 RMAFEDIKLGDLIIPKGL 409
                       107 D-AFQE-ELQELGIPODL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z29443; CAA82571.1;
HSSP; P79134; IAVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                              01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                       PRELIMINARY;
                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                  NEX-2 PROTEIN.
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P72747;
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027512
027512;
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MEDLINE: 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURKOND J., CONNELL M., COPSET T., COOPER J., COULSON A.,
BONFIELD J., BURKON J., LONNELL M., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
ILGHTNING J., LLOYD C., MCMORRAY A., MORTIMORE B., O'CALLAGHAN M.,
LIGHTNING J., PERCY C., RIFKEN L., ROOPEN A., SAUNDERS D., SHOWNKEEN R.,
SMALLON N., SMITH A., SONNHAAMER E., STADEN R., SULSTON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
PARSON B., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                STRAIN-PCC6803;
MEDLINES, 97061201.
MEDLINES, 97061201.
MINATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MINAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MINAJIMA N., HIROSAWA M., SUGIURA M., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YANADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 RRAIEQLATIGVNLSLDDFGIGL-GTLSCLQQ-FKIPAVKIH-ESFIKDLEQSPVNEAII 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D90900; BAA16762.1; - PFAM; PF00956; DNF9; 1.
PFAM; PF00990; DNF9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.1%; Score 110; DB 2; Length 706; Best Local Similarity 27.7%; Pred. No. 2.64e-01; Matches 23; Conservative 29; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AINSCOUGH R.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                  to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 706 AA; 79831 MW; 706E0D1E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 AA.
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EMBL; 283317; CABO5899.1; -.
PFAM; PF00751; DM-domain; 1.
SEQUENCE 470 AA; 51820 MW;
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07,
12,
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Caenorhabditis elegans.
                                                        Submitted (JUN-1996)
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STRAIN-PCC6803;
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                          358 ALSNLSAGQELSSFILHSVVLQAQQAQQKTAQQLIPTSM-PSELESTLSLLRLQQSSLGD 416
                                   IGLTIDEAMSDVNQILELVNSVESDQFKKHSIGFFRGILSSKHLERESRDPWLGKVLNVS 270
                                                                                                                                                                                                        COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                 4.
                                                     417 LIKLS-GIQLPTLPTTQPMLTPQMPTLPMMQKALPTVLPGSFQP-FLQPTLF 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 EEHLASITSGLQPLIKASDHLETVNDKLMSVRPNALSRSLGYFQSFVTTMSS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 913;
                48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Score 107; DB 5; Length 913
Pred. No. 6.02e-01;
36; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                   (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 Score 107; DB 5; 1
Pred. No. 6.02e-01;
30; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U50069; AAB37561.1; -.
SEQUENCE 913 AA; 103125 MW; 2D649BD4 CRC32;
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                                                                                                 913
                                                                                                              Created)
                                                                                                PRT;
Query Match
Best Local Similarity 26.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 23.28;
les 26; Conservative
                                                                                                PRELIMINARY;
                                                                                                           01-MAY-1997 (TrEMBLrel
01-MAY-1997 (TrEMBLrel
01-NOV-1998 (TrEMBLrel
                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                               Submitted (MAR-1996)
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
Submitted (DEC-1996;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
BRADSHAW H.;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                           WATERSTON
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P90742
P90742;
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Matches
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150 QTGTTSAAATDRVTISISGLSTL--KTI-MSNATLKVATSTDALKALSTINKÄLTGINTT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of a Molluscum contagiosum virus DNA region which includes the gene encoding protein kinase 2 and other genes with
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCO13L OR B-M,N,L.3.
Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                          mobilis.";
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                                                                                                                                                              group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 RAGLGASESRLSSVVNNLTINVTNLSDARSRIQ-DIDYSSETTNLARSQILSÖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
Z
                                                                                                                                                                                                                                                                                                                                                                       Length 279
                                                                                                                                                                                                                                                                                                                                                                   Score 105; DB 2; Length 279
Pred. No. 1.03e+00;
36; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARTIN-GALLARDO A., MORATILLA M., FUNES J.M., AGROMAYOR M. VARAS A.J., COLLADO M., VALENCIA A., LOPEZ-ESTEBARANZ J.L.
                                                                                                                                                                                                                     SECUENCE FROM N.A.
MORATILLA M., AGROMAYOR M., NUNEZ A., FUNES J.M., VARAS
LOPEZ-ESTEBARANZ J.L., ESTEBAN M., MARTIN-GALLARDO A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Zymomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SENKEVICH T.G., BUGERT J.J., SISLER J.R., KOONIN E.V.,
                                                          Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 AA.
                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98184; 012880; 012599;
01-FEB-1997 (TEMBLEEL 02,
01-FEB-1997 (TEMBLEEL 02,
01-NOV-1999 (TEMBLEEL 12,
MC013L.
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.0%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unique organization.";
Virus Genes 13:19-29(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:813-816(1996).
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                        Zymomonas.
                                                                                           FLAGELLIN.
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Q98184
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"A set of ordered cosmids and a detailed genetic and physical map for
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302 AA; 33005 MW;
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
DODD I.B., EGAN J.B.;
"Bacteriophage 186 complete
Submitted (OCT-1995) to the
                                                                                                                                                                                                                                                                                                                                            to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match
Local Similarity 25.2%;
hes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                             XUE Q., EGAN J.B.;
Submitted (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q9X7Y2
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                                                                                                                                                                                                                                                                    132 EAVEGLERVLHLPGGRLLIVELAPFQALETRSLRFPGYGLHYSGMAGELRVALRVRVPDA 191
                                                                                                                                                                                                                                                                                               KEWARRANGI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,
JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
HOSOTANA A., FUKUI S., NAGAI Y., NISHIJIMA K., NKKAZAWA H.,
TAKAMIYA M., MASUDA S., FUKHASHI T., TANAKA T., KUDOH Y.,
YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
NOMURA N., SAKO Y., KIKUCHI H.;
"Complete genome sequence of an aerobic hyper-thermophilic
pra Res. 6.83-101(1999).
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MORATILLA M., AGROMAYOR M., NUNEZ A., FUNES J.M., VARAS A.J.,
LOPEZ-ESTEBARANZ J.L., COLLADO M., PAVON M., MARTIN-GALLARDO A.;
SUBMILTACE (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U60315; AAC55414.1; -.
EMBL; U86894; AAB57933.1; -.
EMBL; U86894; AAB57933.1; -.
EMBL; PSS685; LHDJ.
SEQUENCE Z26 AA; 25301 MW; 584D5F47 CRC32;
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Pred. No. 1.35e+00;
22; Mismatches 33; Indels
                                                                                                                                                                                     Length 226;
                                                                                                                                                                                     Score 104; DB 14; Length 220
Pred. No. 1.35e+00;
23; Mismatches 34; Indels
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
228AA LONG HYPOTHETICAL PROTEIN.
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SEQUENCE 228 AA; 25890 MW; A421A9B2 CRC32;
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Archaea; Crenarchaeota; Aeropyrum.
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SEQUENCE OF 241-302 FROM N.A.
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Local Similarity 32.2%;
les 29; Conservative
                                                                                                                                                                                       Match 6.7%;
Local Similarity 30.3%;
hes 27; Conservative
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09YBI8;
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OLIVER K., HARRIS D.; "A set of ordered cosmids and a detailed genetic and physical map for
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XUE Q.; "Studies on the tail region of the temperate coliphage 186 genome."; Thesis (1993), University of Adelaide, Australia.
                                                                                     SECUENCE FROM N.A.
MEDLINE; 98371265.
PORTELLI R., DODD I.B., XUE Q., EGAN J.B.;
"The late-expressed region of the temperate coliphage 186 genome.";
Virology 248:117-130(1998).
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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MEDLINE: 9700351.
REDERINA: M. KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KINASHI H., HOPWOOD D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 302
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 1.35e+00;
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37; Mismatches
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                                                                                                                                                                  240 GNLAQERLAIAV-GAAAATEEILDITTRYVKEREAFGRPLAKLQHVRFEIAEMATEA-AV 297
                                                                                                                                                                                      272 DLSHNRVAGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAINFISHER,
MEDLINE: 98121980.
DELHNATY P. J., BAXTER R.C.;
Cloning and characterization of the rat gene for the acid-labile subunit of the insulin-like growth factor binding protein complex.";
J. Mol. Endocrinol. 19:267-277(1997).
EMBL: AF006203; AAC15252.1;
                                                                                                                                                  Gaps
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID-LABILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104; DB 11; Length 603;
Pred. No. 1.35e+00;
31; Mismatches 36; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                  Length 382;
                                                                                                        Query Match 6.7%; Score 104; DB 2; Length 382
Best Local Similarity 27.2%; Pred. No. 1.35e+00;
Matches 28; Conservative 27; Mismatches 41; Indels
the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL: AL049485; CAB39720.1, ...
PROSITE; PS00072; ACYL_COA_DH_1; 1.
PROSITE; PS00073; ACYL_COA_DH_2; 1.
SEQUENCE 382 AA; 42143 MM; 4E2F94FE CRC32;
                                                                                                                                                                                                                           298 TRIFLDRCVIEHVAGRLDPVHASMAKWWA-TELQKRVVDRCLQ 339
                                                                                                                                                                                                                                                | :|| |::: :: | | | :|:
134 QRPLLDS-VAQQQGSSL-P-HVSYFRWRVDVAISTSAQSRSLQ 173
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PFAM; PF01560; LRR; 19.
PFAM; PF01462; LRRT; 1.
PRINTS; PR00019; LEURICHRPT.
SEQUENCE 603 AA; 66924 MW; 74E63165 CRC32;
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                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 31.9%;
Matches 38; Conservative
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Search completed: Fri May 12 10:25:41 2000 Job time : 87 secs.

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protein - protein database search, using Smith-Waterman algorithm Fri May 12 10:23:17 2000; MasPar time 34.78 Seconds 192.339 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

>US-09-223-796-2 (1-224) from US09223796.pep 1552

Description: Perfect Score: Sequence:

1 MSALGAAAPYLHHPADSHSG......ALVLKEMAELEKKCERKLQD 224

PAM 150 Gap 11 Scoring table:

82229 seqs, 29864866 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Statistics:

swiss-prot38 1:swissprot

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 47.784; Variance 95.999; scale 0.498

SUMMARIES

	Pred. No.	3.38e-03	2.14e-02	3.92e-02	2.30e-01	4.08e-01	4.08e-01	5.43e-01	7.20e-01	5.43e-01	7.20e-01	7.20e-01	1.26e+00	1.26e+00	1.66e+00	1.26e+00	2.18e+00	2.18e+00	2.87e+00	2.87e+00	2.87e+00	3.75e+00	4.91e+00	6.40e+00
	Description	TUMOR NECROSIS FACTOR	BASEPLATE ASSEMBLY PRO	BS4 PROTEIN.	CHROMOSOME SEGREGATION	INSULIN-LIKE GROWTH FA	HYPOTHETICAL 98.0 KD P	NUCLEOCAPSID PROTEIN (CHAPEONE PROTEIN HSCC	HYPOTHETICAL 65.0 KD P	INSULIN-LIKE GROWTH FA	INSULIN-LIKE GROWTH FA	HYPOTHETICAL TRANSCRIP	HYPOTHETICAL 89.3 KD P	PROTEIN KINASE C-LIKE	RNA-DIRECTED RNA POLYM	INSULIN-LIKE GROWTH FA	PUTATIVE TRANSLATIONAL	MYELOMONOCYTIC GROWTH	HYPOTHETICAL 66.8 KD P	TRANSCRIPTION-REPAIR C	CHROMOSOME SEGREGATION	HYPOTHETICAL 7.0 KD PR	NONSTRUCTURAL PROTEIN
	Ü	TRA1_HUMAN	VPJ_BPP2	BS4_MOUSE	SMC2_YEAST	ALS_RAT	YFIQ_ECOLI	NCAP_INSVN	HSCC_ECOLI	YBAE_ECOLI	ALS_MOUSE	ALS_PAPPA	YM50_MYCTU	YBBP_ECOLI	PKL2_RAT	RRPL_PUUMH	ALS_HUMAN	YAQ5_SCHPO	MGF_CHICK	YMB3_YEAST	MFD_MYXXA	SMC3_YEAST	YRKD_BACSU	VNST_BUNSH
	DB	-	Н	-	Н	-1	н	 1	H	-4	-4	Н	-	Н	ч	Н	Н	н	н	ч	Н	Н	Н	٦
	Query Match Length DB	661	302	677	1170	603	886	262	556	266	603	605	219	804	842	2156	605	2670	201	584	1201	1230	63	92
ø	Query	7.7	7.3	7.2	8.9	6.7	6.7	9.9	9.9	9.9	9.9	9.9	6.4	6.4	6.4	6.4	6.3	6.3	6.2	6.2	6.2	6.2	6.1	6.1
	Score	120	114	112	106	104	104	103	102	103	102	102	100	100	66	100	98	86	97	97	97	96	95	94
	Result No.	++	7	m	4	S	φ	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

6.4.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.4.00 6.	8.32e+00 8.32e+00 8.32e+00 1.08e+01 1.08e+01 1.08e+01 1.08e+01 1.08e+01
METHIONYL-TRNA FORMYLT DNA PRIBASE (EC 2.7.7. TIMELESS PROTEIN (FRAG SLP1 PROTEIN (VACUCLAR PROTEIN KINASE YAKI (E UBIQUITIN CARBOXYL-TER XANTHINE DEHYDROGENASE DYNEIN BETA CHAIN, FLA KAFIRIN PGKI PRECURSOR COPPER TRANSPORT ATP-B ACETYL-COENYZWE A CARB GLUTAMATE 5-KINASE (EC	ADENYLOSUCCINATE LYASE GLYCEROL-3-PHOSPHATE D RAB6-INTERACTING KINES ZINC FINGER PROTEIN GL HYPOTHETICAL 43.6 KD P MATURATIVE MOLYBDENUM TR HYPOTHETICAL 56.4 KD P NUCLEAR PORE COMPLEX P NUCLEAR PORE COMPLEX P
PRIM_MYXXA PRIM_MYXXA TIM_DROHY SLP1_YEAST YAK1_YEAST XDH_EMENI DYHE_GHLME KAF1_SORBI NOSF_PSEST ACCA_HAETH PROB_METRU	BPURB_HABEIN GPDM_MOUSE RB6K_MOUSE GLI1_HUWAN YEAR_ECOLI PIVZ_ADB1Z MODF_ECOLI YIEN_ECOLI NI55_HUWAN NTC1_HUWAN
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ALIGNMENTS

MEDLINE; 9181307.
SONG H.Y., DUNBAR J.D., ZHANG Y.X., GUO D., DONNER D.B.;
"Identification of a protein with homology to hsp90 that binds the type 1 tumor necrosis factor receptor.";
J. Biol. Chem. 270:3374-3381(1995). TRA1_HUMAN STANDARD; PRT; 661 AA.
12.19131; 075235;
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN (TRAP-1) Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. SEQUENCE FROM N.A. MEDLINE; 95181307.

RICKE D.O., BRUCE D., MUNDT M., DOGGETT N., MUNK C., SAUNDERS E., RICKE D.O., BRUCE D., MUNDT M., DOGGETT N., MUNK C., SAUNDERS E., ROBINSON D., JONES M., BUCKINGHAM J., CHASTEER L., THOMPSON S., GOODWIN L., BRYANT J., MEINCET J., MALTBIE M., MISTA M., UENG S., TATUM O., CAMPBELL C., FAWCETT J., MALTBIE M., MISRA M., DEAVEN L.;
SLUMITE G. (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-I. FUNCTION: BINDS TO THE INTRACELLUAR DOMAIN OF TUMOR NECROSIS FACTOR TYPE I RECEPTOR.

-I TISSUE SPECIFICITY: FOUND IN SKELETAL MUSCLE, LIVER, HEART, BRAIN,

KINDEY, PANCREAS, LUNG AND PLACENTA.

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-> R (IN REF. 2).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 GNVDHAATHISNRREELAQIRKE-EKEKRRRLE-NVNTLRGMGYSTQAAKQALHQARGN 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 L-DDALKVLLSNPHMWWLQDADP-ENNSRQASPSQESINQLVYMGFDTVVAEAALRVFGG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 LSEERLAVLLAGTHTL-LQQALRLPPASLKPDAFQEELQELG-IPQDLIGDLASL-AFGS 133
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STRAIN=S288C / AB972;
MEDLINE; 96287654.
EXI I., NAITOU M., HAGIWARA H., ABE M., OZAWA M., SASANUWA S.-I.,
SASANUWA M., TSUCHIYA Y., SHIBATA T., WIANABE K., ONO A.,
YAWAZAKI M.-A., TASHIRO H., HANAOKA F., MURAKAMI Y.;
"Fifteen open reading frames in a 30.8 kb region of the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 GRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALHGKDCR-EAVEQ-L-GASAN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 112; DB 1; Length 677;
Pred. No. 3.92e-02;
29; Mismatches 59; Indels 10;
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MEDLINE; 95400292.
MEDLINE; 95400292.
MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,
SASANUMA S.-I., SASANUWA M., TSUCHIYA Y., SOEDA E., YOKOYAMA FAMAZAKI M., TASHIRO H., EKI T.;
"Analysis of the nucleotide sequence of chromosome VI from Saccharomyces creevisiae.";
Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUNNIKOV A.V., HOGAN E., KOSHLAND D.; "SMC2, a Saccharomyces cerevisiae gene essential for chromos segregation and condensation, defines a subgroup within the family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEE-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CHROWOSOME SEGREGATION PROTEIN SMC2 (DA-BOX PROTEIN SMC2)
                                                                                                   SHAN B., PARSA A.T., LEWIS J.A.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
-1- INDUCTION: BY INTERFERON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 AA; 77448 MW; A0235186 CRC32;
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larity 28.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 ORPLIDSVAQQQGSSLP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 NVQLAAQTLAHHGGSLP 533
                                                                         IISSUE-CONNECTIVE TISSUE;
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les 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMC2 OR YFR031C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMC2_YEAST
P38989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                      80 KKLLDIVARSLYS-E-KEVFIRELISNASDALEKLRHKLVSDGQALPEMEIHLQTNAEKG 137
                                                                                                                                                                                                                                                     RKLLKLVVGALHGKDCREA-VEQLGASANLSEERLAV-LLAGTHTLLQQALRLPPASLKP 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 NGEDVRPVADRVTVQSAAIVEYQINATLYLYPGPESEPIR-AAAVKKLEAYITAQHRLGR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 HGKDCREAVEQLGA-SANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUNSHINE M.G., LINDQVIST B.H., KIM K.-J., BARREIRO V., KOONIN E.V., CALENDAR R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAGGARD-LJUNGQUIST E., JACOBSEN E., RISHOVD S., SIX E.W., NILSSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage P2.
Viruses; dsDNA viruses, no RNA stage; Talled phages; Myoviridae.
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9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Bacteriophage P2: genes involved in baseplate assembly.";
Virology 213:109-121(1995).
-1- FUNCTION: LIES AT THE EDGE OF THE BASEPLATE.
                                                                  Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 302;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                    TITIQD-TGIGMTQEELVSNLGTIARSGSKAFLDALQNQAEAS 179
                                                                                                                                                                                                                                                                                                                                                     107 DAFQEELQELGIPQD-LIGDLASLAFGSQRPLLDSVAQQQGSS 148
                                                           Score 120; DB 1; Le:
Pred. No. 3.38e-03;
40; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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   055E95AF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF063097; AAD03284.1; -. SEQUENCE 302 AA; 32780 MW; CB8BBA88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
BASEPLATE ASSEMBLY PROTEIN J (GPJ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
BS4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 AA
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01-OCT-1996 (Rel. 34, Last seq
15-DEC-1999 (Rel. 39, Last ann
   75342 MW;
                                                           Query Match 7.7%;
Best Local Similarity 22.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD:
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   661
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BS4_MOUSE
P54729;
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VPJ_BPP2
P51767;
SEQUENCE
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Matches
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         ä
chromosome VI from Saccharomyces cerevisiae.";
Yeast 12:177-190(1996).
-!- FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS. COULD BE PART OF A CHROMOSOME CONDENSATION MOTOR.
-!- SUBBUILT: HOMODIMER OR HETERODIMER WITH SMC1 OR OLIGOMERS.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DOMAIN: CONSISTS OF TWO PUTATITY CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAI J., BAXTER R.C.; "Molecular cloning of the acid-labile subunit of the rat insulin-like growth factor binding protein complex."; Biochem. Biophys. Res. Commun. 188:304-309(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                          796 LKKELKLLAKELEEQESESERKYDLFQNLELETEQLSSELDSNKTLLHNHLK-SIESLKL 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALS_RAT STANDARD; PRT; 603 AA.
P35625;
P356327;
C1-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN IGFALS OR ALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAXTER R.C., DAI J.;
"Purification and characterization of the acid-labile subunit of rat serum insulin-like growth factor binding protein complex.";
Endocrinology 134:848-852(1994).
-i- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF
                                                                                                                                                                                                                                                                                                                                                                              Score 106; DB 1; Length 1170;
Pred. No. 2.30e-01;
21; Mismatches 44; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
MW; C8865ACO CRC32;
                                                                                                                                                                                                                                                                                            coil; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 ENSDLEGKIRGVEDDLVTVQTELN-EEKKRLMD 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 24-44, AND CHARACTERIZATION.
STRAIN=WISTAR; TISSUE=SERUM;
MEDLINE; 94130835.
BAXTER R.C., DAI J.;
                                                                                                                                                                                                                                                     PIR; $48530; $48530.
HSSP; P02633; 1B0D.
SGD; L0001927; SMC2.
Mitosis; ATP-binding; Coiled cc
NP_BIND 32 39 AJ
                                                                                                                                                                                                                   EMBL; U05820; AAA17416.1; -.
EMBL; D50617; BAA09270.1; -.
EMBL; D44602; BAA08042.1; -.
                                                                                                                                                                                                                                                                                                                                           1093 1119
1170 AA; 133927
                                                                                                                                                                                                                                                                                                                                                                              / Match 6.8%;
Local Similarity 26.9%;
nes 25; Conservative
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MEDLINE; 93038676.
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CIRCULATING IGFS TO THE TISSUES.
SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 KD WITH IGF-I
OR IGF-II AND IGFB-3.
SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 DLSHNRVAGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 RIFEGLGQLEVL-TLNDNQITEV-RVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 20.
                                                                                                                                                                   -!- TISSUE SPECIFICITY: BRAIN, KIDNEY, LUNG, HEART, SPLEEN, MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN. LEUCINE-RICH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches 36; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Leucine-repeat; Repeat; Signal. SIGNAL 1 23 INSULIN-LIKE GRO CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S46785; CAB29017.1; -.
PIR; JC1282; JC1282.
HSSP; P23945; IXUN.
PFAM; PF00560; LRR; 19.
PFAM; PF01462; LRRNT; 1.
PFAM; PF01463; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66811 MW;
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Best Local Similarity 31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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603 AA;
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P76594; Q47320;
                                                                                                                                                                                                              AND LIVER
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FUNCTION: ENCAPSIDATES THE RNA.
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                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 RLFSEAGLPTYRTPEGTITAFMHMVEYRRNQKQLRETPALPSN-LTSNTAEAHLLLLQQAI 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                      SEQUENCE FROM N.A.
STRAINKIZ 7 MG1655;
MEDLINE; 97426617
BLATINE; 974267
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRRPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                   NASHIMOTO H., SAITO N.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, IN THE N-TERMINAL, TO SUCCINYL-COA LIGASES.
-!- SIMILARITY: STRONG, TO M.JANNASCHII MJ0590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE HANN, P., DE AYLLA A.C., KORMELINK R., WESTERBROEK A., GIELEN J.J.L., PETERS D., GOLDBACH R.; The nucleotide sequence of the S RNA of Impatiens necrotic spot virus, a novel tospovirus."; FEBS Lett. 306:27-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Impatiens necrotic spot virus (strain NL-07) (INSV).
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 98.0 KD PROTEIN IN UNG-PSSA INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 886;
                                                                                                                                                                              MAU B., SHAO Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ST -> YA (IN REF. 2).
5D400142 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 104; DB 1; 1
Pred. No. 4.08e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
NUCLEOCAPSID PROTEIN (NUCLEOPROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ECOGENE; EG14224; YFIQ.
PFAM; PF00583; Acetyltransf; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D64044; BA10925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 AEGATSLDTHEVQPILQAYGM 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 RLPPASLKPDAFQEELQELGI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 886 AA; 97987 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match
Local Similarity 27.2%;
hes 22; Conservative
                                                                                                                                                                                                                              SEQUENCE OF 1-612 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE; 92331780.
                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCAP_INSVN
Q01808;
                                                                                                                                                                                                                                           STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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YOSHIMUNE K., YOSHIMURA T., ESAKI N.;
"HSe62, a new DnaK homologue of Escherichia coll.";
Biochem. Biophys. Res. Comunu. 250:115-118(1998).
-i- FUNCTION: PROBABLE CHAPERONE. HAS ATPASE ACITIVITY. NOT STIMULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIN D.,
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MEDLINE; 97061202.
MEDLINE; 97061202.
OSHIMA T., IABA T., FUJITA K., HAYASHI K., HONJO A., OSHIMA T., IABA T., ITOH T., KAJIHARA M., KANAI K., KASHIMOTO K., IMADA T., ITOH T., KAJIHARA M., MIKI T., MIZOBUCHI K., MORIH H., MOTOMURA K., NKAMURA Y., NASHIMOTO H., NISHIO Y., SAITO N. SAMEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M., HORIUCHI T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
MELLATHERE F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAXHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 103; DB 1; Length 262
Pred. No. 5.43e-01;
12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 ATTDLKSCVLGVLLGGSLPLIASVLNFEIAALVPAIYQDAKHVELGI 183
                                                                                                                                                                                                                                                                                                         PEAM; 923159; S23159.
PFAM; PF01533; Tospo_nucleocap; 1.
Nucleocapsid; RNA-binding.
PAG: 262 AA; 28718 MW; 1B526B0F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSCC_ECOLI STANDARD; PRT; 556 AA. P7319; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1999 (Rel. 39, Last annotation update) CHAPEONE PROTEIN HSCC (HSC62).
                                                                                                                                                                                                                                                                                   EMBL; X66972; CAA47383.1; -. PIR; S23159; S23159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 6.6%;
Local Similarity 36.2%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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125 IPYYR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IT 10
ALS_MOUSE
P70389;
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                                                                                                                                                                                                                                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                             EDLWLPLLNRLRV-PIEQALRDARLKPSQIDSLVLVGGASQMPLVQRIAVRLFGKLPYQS 327
                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILNE: 9742617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAVIS K.,
KURDI O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
ROBERTS D., ALLEN E., ARAUJO R., APARICIO A., CHUNG E., DAVIS
DUNGAN M., EEBERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI
LEW H., LIN D., NAMATH A., OEFNER P., SCHRAMM S., DAVIS R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P46890; P77158;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 65.0 KD PROTEIN IN HUPB-COF INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                         Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                      Score 102, DB 1; Length 556
Pred. No. 7.20e-01;
33; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HATADA E., OHMORI H., OIAO Y., TSUJI M., FUKUDA R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 328 YDPSTI-VALGAAIQAACRLRSEDIEEVILTDICPYSLGVEVNR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                    44794D92 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 AA
                                                                                                                                                                                                                                                               PFAM; PF00012; HSP70; 1.
Chaperone; ATP-binding.
SEQUENCE 556 AA; 61986 MW;
                                                                                                                                      EMBL; AE000169; AAC73751.1; -.
                                                                                                                                                                                          HSSP: P19120; 1ATS.
ECCGENE: EG13653; HSCC.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                    U82598; AAB40851.1; -. D90705; BAA35302.1; -. D90704; BAA35297.1; -.
                                                                                                                                                                                                                                                                                                                        6.68;
                                                                                                                                                                                                                                                                                                                                  Local Similarity 23.1%;
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-358 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12 / MC4100;
PATZER S.I., HANTKE K:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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-! FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF CIRCULATING IGFS TO THE TISSUES.

-! SUBDINI: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 KD WITH IGF-I OR IGF-II AND IGFBP-3 (BY SIMILARITY).

-! SUBCELLULAR LOCATION: EXTRACELULAR.

-! SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 LRFLVTPESLRNAMMEQAL-ETGKQQDVL-ELAQLAPGELRTLLQPFMGGQWQNDTPTLR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
1NSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN
IGFALS OR ALS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOISCLAIR Y.R., SETO D., HSIEH S., HURST K.R., OOI G.T.; "Organization and chromosomal localization of the gene encoding the mouse acid labile subunit of the insulin-like growth factor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 103; DB 1; Length 566;
Pred. No. 5.43e-01;
16; Mismatches 19; Indels
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                            l protein.
566 AA; 64991 MW; 091FA6F1 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
Submitted (OCT-1995) to the EMB-1- SIMILARITY: TO E.COLI YABN.
                                                                                                                                                                                                                                                                                                       CAMPILLE CONTROL CAMPILLS ...
PFAM; PF00496; SBP_bac_5; 2.
Hypothetical protein.
                                                                                                                                                                                                                                                  EMBL; AE000151; AAC73548.1; -.
                                                                                                                                                                                                                                                                           EMBL; U82664; AAB40201.1; -.
EMBL; D82943; BAA11649.1; -.
EMBL; 254355; CAA91182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U66900; AAB17270.1; -.
MGD; MGI:107973; IGFALS.
PFAM; PF00560; LRR; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 6.6%;
Local Similarity 35.4%;
nes 23; Conservative
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Pred. No. 7.20e-01;
28; Mismatches 40; Indels 14; Gaps 13;
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MEDLINE; 97040714.

DELHANTY P., BAXTER R.C.;

DELHANTY P., BAXTER R.C.;

"The clouding and expression of the baboon acid-labile subunit of the insulin-like growth factor binding protein complex.";

Blochem. Biophys. Res. Commun. 227:897-902(1996).

-i- FUNCINON: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS THAT RESULT IN PROTEIN COMPLEXES, RESEPPON-LICAND BINDING OR CELL ADHESION.

-I- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 KD WITH IGF-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 DLSHNRVAGLLEDTFPGLLGLHVLRLAHNAITSLRPRTFKDLHFLEELQLGHNRIRQLGE 331
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUJ-1998 (Rel. 36, Last annotation update)
INSULIN-LIEG GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN
IGFALS OR ALS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 KTFEGLGQLEVL-TLNDNQIHEVKVGAFFGLFNVAV-MNLSGNCLRSLPEHVFQGLGRL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paplo paplo (Guinea baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae,
                                                          INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN. LEUCINE-RICH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
11ADB606 CRC32;
                                Repeat; Signal.
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                                               SIMILARITY
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PFAM; PF01463; LRRCT; 1.
Glycoprotein; Leucine-repeat;
SIGNAL 1 23 B
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les 37; Conservative
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368
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493
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603 AA;
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TISSUE-LIVER;
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ALS_PAPPA
002833;
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Mismatches 37; Indels 14; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 DLSHNRVAGLLEDTFPGLLGLRVLRLSHNAIASLRPRTFEDLHFLEELQLGHNRIRQLAE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 RSFEGLGQLEVL-TLDHNQLQEV-KVGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKL 388
OR IGF-II AND IGFBP-3 (BY SIMILARITY).
SUBCELTULAR LOCATION: EXPRACELLULAR.
SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN
MANY PROTEINS. NUMBER IN THIS PROTEIN: 20.
                                                                                                                                                                                                                                                                                                                               Repeat; Signal.
BY SIMILARITY.
INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN COMPLEX ACID LABILE CHAIN.
LEUCINE-RICH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 1; Length 605
Pred. No. 7.20e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
5DF04D42 CRC32;
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PFAM; PF00560; LRR: 19.
PFAM; PF01462; LRRUT; 1.
PFAM; PF01463; LRRCT; 1.
GlyCoprotein; Leucine-repeat; R
SIGNAL 1 27 BY
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Best Local Similarity 32.8%;
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Hypothetical
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PKL2_RAT
008874;
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                                                 STRAIN-H37RV;

MEDLINE; 9829987.

A GORDON S.V., BROSCH R., FARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKALA F., BACKLOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., BACCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., HOLLING K., FELTWELL T., GENTLES S., HAMLIN N., HOLLOYD S., A DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., MORPHY L., OLLYER S., OSBORNE J., OUAIL M.A., RAJANDREAM M.A., ROGERS J., A RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E., Deciphering the blology of Mycobacterium tuberculosis from the complete genome sequence.";

TOOMPLES S., SELECT K., MALTEHEBL B.C., ELL SIMILARIY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
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                                                                                                                                                              д.
Б.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 VDYGVDRVTLAEIARRAGVSRPTV-YRRWPDTRSIMASMLTSHI-ADVLREVPLDGDDRE 111
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STRAIN-KIZ. / MG1655;
STRAIN-KIZ. / MG1655;
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAXHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAVIS K.,
KURDI O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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1-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 89.3 KD PROTEIN IN TESA-RHSD INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                 62 81 H-T-H MOTIF (BY SIMILARITY).
219 AA; 23875 MW; F3F30AD6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
ROBERTS D., ALLEN E., ARAUJO R., APARICIO A., CHUNG E.,
DUNCAN M., FEDERSPIEL N., HYMAN R., KALMAN S., ROMP C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 1; Pred. No. 1.26e+00; 20; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01081; HTH_TETR_FAMILY; FALSE_NEG. PFAM; PF00440; tetr; 1. Hypothetical protein; Transcription regulatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 6.4%;
Local Similarity 25.6%;
es 23; Conservative
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                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           REGULATORS
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YBBP_ECOLI
P77504;
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SEQUENCE
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Matches
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15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PROTEIN KINASE C-LIKE 2 (EC 2.7.1.-) (PROTEIN-KINASE C-RELATED KINASE
PROTESAE-ACTIVATED KINASE 2) (PAK-2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 ILINVLRRMTLKSLPLRLAVSRIL-RQPWSTLSQLSAFS-LSFMLIALILIVLRGDLLDRWQ 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YO W., LIU J., MORRICE N.A., WETIENHALL R.E.H.;
Isolation and characterization of a structural homologue of human
PRK2 from rat liver: distinguishing substrate and lipid activator
specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEW H., LIN D., NAMATH A., OFFNER P., SCHRAMM S., DAVIS R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 272:10030-10034(1997).
-1- FUNCTION: EXHIBITS A PREFERENCE FOR HIGHLY BASIC PROTEIN SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
TISSUE=MYELOMA, AND LIVER;
MEDLINE; 97248559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 1; L
1.26e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8CE9FA3F CRC32;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                   Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89332 MW;
                                                                                                                                                                                                                                                                                                   U82664; AAB40250.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.48;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                        ECOGENE; EG13263; YBBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700
                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  804 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||| |
97 LRLPPAS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 QQLPPES 489
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331
331
403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 LQAVLTNELAFDNAKPVISPLELRNGRIIEH -- HFRIEFAVAEGAKNYMKLLGSGKVTDR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymerase.";
Virology 183:386-391(1991).
-!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M63194; -; NOT_ANNOTATED_CDS.
PIR; A40319; RRVUNE.
Transferase; Nucleotidyltransferase; RNA-directed RNA polymerase.
SEQUENCE 2156 AA; 247048 WW; DEFC118F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Puumala virus (strain Hallnas B1) (Nephropathia epidemica virus)
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 91272501.
STOHWASSER R., RAAB K., DARAI G., BAUTZ E.K.F.;
"Primary structure of the large (L) RNA segment of nephropathia
epidemica virus strain Hallnas Bl coding for the viral RNA
                                                                                                                                                                                                                                                       EMBL; U75358; AAB53364.1; -. PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PROSITE; PS00107; PROTEIN_KINASE_AIP; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. PRAM: PF00069; PKINASE; 1. PFAM: PF0043; pkinase; 1. PFAM: PF00433; pkinase_C; 1. Transferase; ATP-binding; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99; DB 1; Length 842;
Pred. No. 1.66e+00;
30; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (L PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95650 MW; B4B0C8E1 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 K-LTDGSAHRFEVPIAKFQELRYSVALVLKEMA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 6.4%;
Local Similarity 25.8%;
les 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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527
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842 AA;
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RRPL_PUUMH
P27176;
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ACT_SITE
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Score 100; DB 1; Length 2156; Pred. No. 1.26e+00;

6.4%;

Query Match Best Local Similarity

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6
 1855 LLAHAYHNLKDVRYQALQAVGNVWFKMTQHKLFINPIISAGLLENFMKGLPAAIPPAAYS 1914
 1915 LIMNKAKISVDLFMFNELLAL-INPONVLNLDGIEETSEGYTTVSTISSTQWSEEVSLT 1972
 9; Gaps
 39; Mismatches 43; Indels
 Search completed: Fri May 12 10:23:56 2000 Job time : 39 secs.
 Conservative
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 Matches
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri May 12 10:25:59 2000; MasPar time 53.66 Seconds 196.913 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-223-796-2 (1-224) from USO9223796.pep 1552 1 MSALGAAAPYLHHPADSHSG.....ALVLKEMAELEKKCERKLQD 224

Title: Description: Perfect Score: Sequence:

**PAM** 150 Gap 11 Scoring table:

142080 segs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 46.684; Variance 106.313; scale 0.439 pir62 1:pirl 2:pir2 3:pir3 4:pir4 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Š.                         | e-02                 | 2.01e-02              | 51e-02               | 12e-01 | 92e-01 | 92e-01               | 99e-01                | 51e+00               | 51e+00 | 51e+00 | 51e+00 | 52e+00 | 96e+00 | 52e+00               | 96e+00                | 52e+00                | 96e+00                | 52e+00                | 52e+00                | .19e+00              | 19e+00                | .38e+00              | 196+00                |
|----------------------------|----------------------|-----------------------|----------------------|--------|--------|----------------------|-----------------------|----------------------|--------|--------|--------|--------|--------|----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|----------------------|-----------------------|----------------------|-----------------------|
| Pred.                      | 1.52e-02             | 2.01                  | 3.51                 | 3.12   | 6.92   | 6.92                 | 8.99                  | 1.51                 | 1.51   | 1.51   | 1.51   | 2.52   | 1.96   | 2.52                 | 1.96                  | 2.52                  | 1.96                  | 2.52                  | 2.52                  | 4.19                 | 4.19                  | 5.38                 | 4 19                  |
| Description                | hypothetical protein | tumor necrosis factor | hypothetical protein |        |        | hypothetical protein | chromosome segregatio | hypothetical protein |        |        |        |        | c      | hypothetical protein | fructose-6-p phosphot | probable dnaK-type mo | probable membrane pro | insulin-like growth f | insulin-like growth f | hypothetical protein | probable histidine de | hypothetical protein | probable membrane pro |
| Q.                         | 875449               | A55877                | S41022               | S74610 | T11778 | T15474               | A56157                | E72540               | JC1282 | G65036 | S77213 | T05656 | S23159 | S74728               | F72111                | H64799                | E64774                | JC6128                | JC5239                | E70779               | D72734                | S76863               | G64780                |
| BB                         | 7                    | 7                     | N                    | ~      | ~      | ~                    | N                     | ~                    | ~      | ~      | N      | ~      | ď      | 7                    | N                     | ~                     | ~                     | ~                     | ~                     | ~                    | ~                     | ~                    | ~                     |
| %<br>Query<br>Match Length | 491                  | 661                   | 9/9                  | 206    | 668    | 913                  | 1170                  | 228                  | 603    | 988    | 1116   | 159    | 262    | 451                  | 552                   | 556                   | 266                   | 603                   | 605                   | 219                  | 362                   | 371                  | 804                   |
| %<br>Query<br>Match        | 7.8                  | 7.7                   | 7.6                  | 7.1    | 6.9    | 6.9                  | 9.8                   | 6.7                  | 6.7    | 6.7    | 6.7    | 9.9    | 9.9    | 9.9                  | 9.9                   | 9.9                   | 9.9                   | 9.9                   | 9.                    | 6.4                  | 6.4                   | 6.4                  | 6.4                   |
| Score                      | 121                  | 120                   | 118                  | 110    | 107    | 107                  | 106                   | 104                  | 104    | 104    | 104    | 102    | 103    | 102                  | 103                   | 102                   | 103                   | 102                   | 102                   | 100                  | 100                   | 66                   | 100                   |
| Result<br>No.              | н                    | 7                     | ო                    | 4      | ស      | ø                    | 7                     | <b>ω</b>             | თ      | 10     | 11     | 12     | 13     | 14                   | 12                    | 16                    | 17                    | 18                    | 19                    | 50                   | 21                    | 22                   | 23                    |

#type complete

A55877

RESULT ENTRY

N

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#authors Song, H.Y.; Dunbar, J.D.; Zhang, Y.X.; Guo, D.; Donner, D.B.
journal
J. Biol. Chem. (1995) 270:3574-3581
#fitle Identification of a protein with homology to hsp90 that binds
the type 1 tumor necrosis factor receptor.
#cross-references MUID:95181307
 .;
 ö
 118 STDFIQKSEDLK-DEEKVALERIVEQKLAESAKNEKDIAWNVNIVVANSYVAKSLRPVIN 176
 59 C-ELVKESRSHEMLSEEQLATLYDCATTSTRLPNDFADDQEDLKNIIRYGELFKACHAIN 117
 80 KKLLDIVARSLYS-E-KEVFIRELISNASDALEKLRHKLVSDGQALPEMEIHLQTNAEKG 137
necrosis factor type 1 receptor associated protein
 Gaps
 841022 #type complete
hypothetical protein 107C4.9 - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
09-sep-1997
 Gaps
 #formal_name Homo sapiens #common_name man
23-Mar-1995_#sequence_revision 23-Mar-1995 #text_change
 ##residues 1-661 ##label SON ##cross-references GB:U12595; NID:9687237 ##cross-references GB:U12595; NID:9687236; PID:9687237 FICATION #superfamily heat shock protein 90 #length 661 #molecular-weight 75342 #checksum 9066
 #checksum 2702
 ë
 #domain annexin repeat homology #label AXI\
#domain annexin repeat homology #label AX6\
#domain annexin repeat homology #label AX3\
#domain annexin repeat homology #label AX4\
#length 676 #molecular-weight 74968 #checksum 2
 Berks, M.
submitted to the EMBL Data Library, January 1994
 ##residues
##ross-references EMBL:Z29443; NID:g1067051; PID:g443836
 Length 661;
 Score 118; DB 2; Length 676;
Pred. No. 3.51e-02;
31; Mismatches 67; Indels
 34; Indels
 138 TITIOD-TGIGMTQEELVSNLGTIARSGSKAFLDALQNQAEAS 179
 69/3; 161/1; 208/3; 227/1; 357/1; 505/3 #superfamily annexin repeat homology
 Query Match 7.7%; Score 120; DB 2; I Best Local Similarity 22.3%; Pred. No. 2.01e-02; Matches 23; Conservative 40; Mismatches 34;
 Score 118;
 IQMPTVGGDTN-FEFDIDSFAQFR 199
 human
 preliminary
 preliminary
 7.6%;
Local Similarity 25.7%;
les 37; Conservative
 26-Aug-1999
 ##molecule_type mRNA
 ##molecule_type DNA
 S41022
S41014
 541022
 A55877
 CLASSIFICATION
SUMMARY
 #introns
 #authors
#submission
 ##status
 #accession
 Query Match
 #authors
#journal
 373-444
445-516
528-600
604-675
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Yang, Y.L.; Goldrick, D.; Hong, J.S.
J. Bacteriol. (1988) 170:4299-4303
Identification of the products and nucleotide sequences of
two requiatory genes involved in the exogenous induction of
phosphoglycerate transport in Salmonella typhimurium.
 (strain PCC
 5
 FRENCE

Raneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;

Rauthors Raneko, T.; Miyaina, N.; Histosa, M.; Suglura, M.;

Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, M.;

Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;

Yasuda, M.; Tabata, S.

#journal DNA Res. (1996) 3:109-136

#title Squence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
 nucleic acid sequence not shown; translation not shown
 585 RRAIEQLATIGVNLSLDDFGIGL-GTLSCLQQ-FKIPAVKIH-ESFIKDLEQSPVNEAII 641
 #formal_name Synechocystis sp.
PCC 680
25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
29-Sep-1999
 5; Gaps
 phosphoglycerate transport regulatory protein pgtB - Salmonella typhimurium #formal_name Salmonella typhimurium 16-Jul-1999 #text_change 16-Jul-1999
 ##residues 1-668 ##label YAN
##cross-references EMBL:M31279; NID:9858752; PID:9858753;
##experimental_source strain LIS
XX #length 668 #molecular-weight 75231 #checksum 5379
 Sp.
 Score 110; DB 2; Length 706;
Pred. No. 3.12e-01;
29; Mismatches 26; Indels
 preliminary; translated from GB/EMBL/DDB;
 Score 107; DB 2; Length 668 Pred. No. 6.92e-01;
 S74610 #type complete
hypothetical protein s1r1103 - Synechocystis
 #type complete
 124 GDLASLAFG-SQRPLLDSVAQQQ 145
 642 TSIMTLGRKLGVRIISEGVETQQ 664
 *cross-references MUID: 88314933
 Ouery Match 7.1%;
Best Local Similarity 27.7%;
Matches 23; Conservative
 Query Match 6.9%;
Best Local Similarity 31.5%;
 ##molecule_type DNA
 ##molecule_type DNA
 S74610
 217339
 T11778
 CLASSIFICATION
 ##status
 #accession
 #accession
 #authors
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 Strunnikov, A.V.; Hogan, E.; Koshland, D. Genes Dev. (1995) 9:887-599
SMC2, a Saccharomyces cerevisiae gene essential for chromosome segregation and condensation, defines a subgroup within the SMC family.
 S56186
Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa,
M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.; Soeda, E.;
 5,
 ņ
 chromosome segregation protein SMC2 - yeast (Saccharomyces
 211 IGLTTDEAMSDVNQILELVNSVESDQFKKHSIGFFRGILSSKHLERESRDPWLGKVLNVS 270
 DA-box protein; protein R003; protein YFR031c; structural maintenance of chromosomes 2
#formal_name Saccharomyces cerevisiae
03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change
 99 DKIERLSQGLQLAERRQLAVILQDSRTLLAELDNALYNWFLVREKVSELSARLTGSSDDF 158
 : :|:|: |:| ||| |||:| ::||| :
66 EAVEQLGASANLSEER-LAVLLAGTHTLLQQ-ALRLPPASLKPDAFQEELQEL-GIPQDL 122
 Gaps
 #checksum 7779
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 υ,
.,
 Submitted to the EMBL Data Library, February 1996
The sequence of C. elegans cosmid C09B9.
 271 EEHLASITSGLQPLIKASDHLETVNDKLMSVRPNALSRSLGYFQSFVTTMSS 322
 ##status preliminary; translated from GB/EMBL/DDBJ#manalated from GB/EMBL/DDBJ#manalat
 Score 107; DB 2; Length 913;
Pred. No. 6.92e-01;
36; Mismatches 45; Indels
 ||:|| : :| : :| : :| EBRLAVILAGTHTLLQQALRIPPASLKPDAFQ-EEL-QELGIPQDLIGDLAS
 758/2; 864/2; 895/2
#length 913 #molecular-weight 103125
 A56157; S56286; S62242; S63836; S48530
Mismatches
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 123 IGDLASLA--FGSQR-PLLDSVAQQGGSS 148
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 1-913 ##label BRA
 18;
 #cross-references MUID:95212908
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Best Local Similarity 23.2%;
Matches 26; Conservative
 20-Sep-1999
 24-Sep-1999
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 CESP: C09B9.7
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Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.;
Haakawa, Y.; Jin-no, K.; Takahashi, M.; Sekine, M.; Baba,
S.; Ankal, A.; Kosugi, H.; Hosoyama, A.; Fukui, S.; Nagai,
Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.;
Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
Kushida, N.; Oguchi, A.; Aoki, K.; Kubota, K.; Nakamura,
Y.; Nomura, N.; Sako, Y.; Kikuchi, H.
 'n
 the right
 B72540 *type complete
hypothetical protein APE1610 - Aeropyrum pernix (strain K1)
#formal_name Aeropyrum pernix
20-Aug-1999 *sequence_revision 20-Aug-1999 #text_change
20-Aug-1999
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PID:d1008633; PID:g893426
##note the nucleotide sequence was submitted to the EMBL Data
Library, July 1995
 nucleic acid sequence not shown; translation not shown
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.
 from
 796 LKKELKLLAKELEEQESESERKYDLFQNLELETEQLSSELDSNKTLLHNHLK-SIESLKL 854
 #domain transmembrane #status predicted #label TMI\
#domain transmembrane #status predicted #label TM2
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 #authors S63830
#authors Eki, T.; Naitou, M.; Hagiwara, H.; Abe, M.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.; Shibata, Matanabe, K.; Ono, A.; Yamazaki, M.A.; Tashiro, H.; Hanaoka, F.; Murakami, Y.
#journal Yeast (1996) 12:177-190
#title Fifteen open reading frames in a 30.8 kb region of the arm of chromosome VI from Saccharomyces cerevisiae.
Yokoyama, K.; Yamazaki, M.; Tashiro, H.; Eki, T. submitted to the EMB1. Data Library, May 1995 Analysis of the nucleotide sequence of chromosome VI Saccaromyces cerevisiae.
 ##cross-references EMBL:D50617; NID:q836685; PIDN:BAA09270.1;
PID:d1009911; PID:g836786; MIPS:YFR031c
 ##residues
##cross-references EMBL:D44602; NID:9893419; PIDN:BAA08042.1;
##cross-references EMBL:D44603; PID:9893426
 э;
т
 Murakami, Y.
submitted to the EMBL Data Library, December 1994
S62242
 conserved hypothetical P115 protein
 Score 106; DB 2; Length 1170; Pred. No. 8.99e-01;
 21; Mismatches 44; Indels
 ##cross-references SGD:S0001927; MIPS:YFR031c
 855 ENSDLEGKIRGVEDDLVTVQTELN-EEKKRLMD 886
 107 DAFQEELQELGIPQDLIGDLASLAFGSQRPLLD 139
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 863836
 E72540
 A72450
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 JC1282 *type complete
insulin-like growth factor-binding protein acid labile chain
 for residue
 #domain signal sequence #status predicted #label SIG\
#product insular-like growth factor binding protein,
acid labile chain #status predicted #label MAT
#length 603 #molecular-weight 66811 #checksum 8075
#journal DNA Res. (1999) 6:83-101
#title Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix K1.
#cross-references WulD:99310339
#accession E72540
 131 VVQLVEKDVKQSPLRRKLQRLKLPDLAAEAYATEGDALAVARELWG-RLARLGAVFRVSI 189
 the authors translated the codon AAG for residue 63
Arg, AAA for residue 205 as Pro and GGT for residu
260 as Arg
*superfamily leucine-rich alpha-2-glycoprotein repeat
 272 DLSHNRVAGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGE 331
 | ||: ||: || || | : :: | 36 VAQLL-KDLDRSTFR-KLLKLVVGALHGKDCREAVEQLGASANLSEERLAVLLAGTH-TL 92
 332 RIFEGLGQLEVL-TLNDNQITEV-RVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKL 388
 #authors Dat, J.; Baxter, R.C.
#journal Blochem Blophys. Res. Commun. (1992) 188:304-309
#fille Molecular cloning of the acidilabile subunit of the rat insulin-like growth factor binding protein complex.
#cross-references MUID:93038676
 Gaps
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30.5ep-1993 #sequence_revision 30-5ep-1993 #text_change
 ##cross-references DDBJ:AP000062; NID:95105244; PIDN:BAA80610.1;
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31; Mismatches 36; Indels 14;
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Matches 29; Conservative 22; Mismatches 33; Indels
 APE1610
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 190 VPSRRLVLAVASPRPDSFGPVVEEVLSIVQ 219
 1-228 ##label KAW
 1-603 ##label DAI
 ##experimental_source liver ##note
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Best Local Similarity 31.9%;
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 ##molecule_type DNA
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 665036
 ##residues
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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 the EMBL Data
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 Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hisosava, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, M.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Nada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Tabata, S.; Tabata, S.; Satorana and S.; Takerobacterium Synochocystis sp. PCC6803: II. Sequence determination of the entire genome and assignment of
 416 RLFSEAGLPTYRTPEGTITAFMHMVEYRRNQKQLRETPALPSN-LTSNTAEAHLLLQQAI 474
 Score 104; DB 2; Length 886;
Pred. No. 1.51e+00;
19; Mismatches 39; Indels 1; Gaps
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
14-Nov-1997
 chain dnax
 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
 #checksum 8010
 col1 K-12
 preliminary; nucleic acid sequence not shown; translation not shown
 #checksum
 the nucleotide sequence was submitted to Library, June 1996
 S77213 #type complete
DNA-directed DNA polymerase (EC 2.7.7.7) III
Synechocystis sp. (strain PCC 6803)
protein s111360
 #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia
#cross-references_MUID:97426617
 ##experimental_source strain K-12, substrain MG1655
X #Iength 886 #molecular-weight 97986 #c
 nucleotidyltransferase
#length 1116 #molecular-weight 122009
 #cross-references MUID:97061201
 _name Synechocystis sp.
 475 AEGATSLDTHEVQPILQAYGM 495
 98 RLPPASLKPDAFQEELQELGI 118
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Best Local Similarity 27.2%;
Matches 22; Conservative
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 G65036
 S74322
 877213
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 ##status
 ##status
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6.7%; Score 104; DB 2; Length 1116;

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#forgation #superfamily tomato spotted wilt virus nucleoprotein N
#length 262 #molecular-weight 28718 #checksum 7578
 S23159
S23158
de Haan, P.; de Avila, A.C.; Kormelink, R.; Westerbroek, A.;
 Gielen, J.J.L.; Peters, D.; Goldbach, R.

#journal FEBS Lett. (1992) 306:27-32

#title The nucleotide sequence of the S RNA of Impatiens necrotic spot virus, a novel tospovirus.

#cross-references MUID:92331780
 Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, February 1999 705656
 622 IAGRENINIDQPALTLVAQIANGGLRDAESLLDQ-LSLLPDLITPDKVWD-LVG-AVPEQ 678
 62 KDCREAVEQLGASANLSEERLAVILAGTHTILQQALRIPPASLKPDAFGEELGEIP-Q 120
 563 LSTAAFNALLKTLEEPPERVVFVLATTDPQ-RVLPTIISRCQRFDYRRIPLQAMVDHLRY 621
 T05656 #type complete
hypothetical protein F22I13.50 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
 4 IGAAA-PYLHHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKL-LKLVVGALHG 61
 Gaps
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 nucleoprotein N - Impatiens necrotic spot virus
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22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change
 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change
23-Jul-1999
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F22113.50
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 Pred. No. 1.51e+00;
34; Mismatches 67;
 30; Mismatches
 : | : |: | : : : : : 188 HRFEVPIA-KFQ-ELRY-SVALVLKEMAELER 216
 81 QE-PTPTSHKLDWEERYLHLQMLLNKLNQSDR 111
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 679 DLLALLEAIASDDAETLLATCRQ 701
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Best Local Similarity 25.0%;
Matches 23; Conservative
Best Local Similarity 24.5%;
Matches 35; Conservative
 20-Sep-1999
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##molecure_rype can 1-451 ##label KAN ##residues 1-451 ##label KAN ##residues = 1-451 ##label KAN ##cross-reference EMBL:D90901; GB:AB001339; NID:g1651897; PID:d1017612; ##cross-reference EMBL:D90901; GB:AB001339; NID:g1651897; PID:d1017612; ##note the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 ##cross-references GB:D26444; NID:q452237; PID:d1006006; PID:q499299
##note the authors translated the codon CCC for residue 236 as
Glu; the authors translated used GTG as an initiation
codon and translated it as Val
the authors say that codon usages suggest this protein
is not expressed at high levels
#length 451 #molecular-weight 49667 #checksum 7763
 4
 ij
 #authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Makazaki, A.; Makazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, S.; Takeuchi, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, S.; Takeuchi, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, S.; Takeuchi, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, S.; Takeuchi, T.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, S.; Takeuchi, S.; Takeuchi, T.; Watanabe, A.; Yamada, M.; Takeuchi, S.; Takeuchi, S.; Takeuchi, S.; Takeuchi, S.; Watanabe, A.; Yamada, M.; Tabata, S.; Takeuchi, S.; Takeuchi
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 'VDPNLEVAQISNRMLQAGGPGLLFENVKG',
'SPFPVAVNLMGTVERICWAMNMDHPLELEDLGKK', 244-451 ##label
 S74728 #type complete
hypothetical protein slr0971 ccmA 3'-region - Synechocystis
sp. (strain PCC 6803)
#formal_name Synechocystis sp.
 #authors Ogawa, T.; Marco, E.; Orus, M.I.
#journal J. Bacteriol. (1994) 176:2374-2378
#title A gene (ccmA) required for carboxysome formation in the
A ganobacterium Synechocystis sp. strain PCC6803.
#cross-references MUID:94209239
 Gaps
 Gaps
 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
 F72111 #type complete
fructose-6-p phosphotransferase - Chlamydia pneumoniae
(strain CML029)
#formal_name Chlamydia pneumoniae
 ;;
 42 ALHFODPRLPEVEQLTLSGT-PEE-LEALALAVETYLQQRLN-PCASLEPSTYPE
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Pred. No. 2.52e+00;
5; Mismatches 21; Indels
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 12; Mismatches 17; Indels
 137 ATTDLKSCVLGVLLGGSLPLIASVLNFEIAALVPAIYQDAKHVELGI 183
Score 103; DB 2;
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 Query Match 6.6%;
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Best Local Similarity 36.2%;
Matches 17; Conservative
 21-Aug-1998
S74728; B55214
 ##molecule_type DNA
 S74322
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##status preliminary ##molecule_type DNA 1-555 ##label ARN ##rosidues 1-555 ##label ARN ##cross-references GB:AE001603; GB:AE001363; NID:g4376422; PID:g4376428 ##experimental_source strain CWL029
 ;
9
6; Gaps
 Score 103; DB 2; Length 555;
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374 NVRVSKIATE-ELLAVMVKKEIEKIKPHMEF 403 

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315 IEHIFDTRKLIDE-LNVLLANGDSSIEKILSKLSPETLKTFHLFPKDIANQLLLARDSHG 373 

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri May 12 10:28:07 2000; MasPar time 17.96 Seconds 161.600 Million cell updates/sec MPsrch\_pp Run on:

Tabular output not generated.

>US-09-223-796-2 (1-224) from US09223796.pep 1552 1 MSALGAAAPYLHHPADSHSG......ALVLKEMAELEKKCERKLQD 224 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

131253 segs, 12956647 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT\_COMB 4:backfiles1

Mean 30.351; Variance 153.535; scale 0.198 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|               |              | de             |           |    |            |              |              |           |
|---------------|--------------|----------------|-----------|----|------------|--------------|--------------|-----------|
| Result<br>No. | t<br>. Score | Query<br>Match | Length DB | DB | Ð          | Description  | _            | Pred. No. |
|               | 1 124        | 8.0            | 195       | 7  | US-08-822- | Sequence 3,  | Applicatio   | 2.71e-01  |
| •             | 2 118        | 7.6            | 195       | ~  | US-08-822- | Sequence 1.  | Applicatio   | 7.00e-01  |
| •             | 3 104        | 6.7            | 603       | ч  | US-08-190- | Sequence 50, |              | ω.        |
| •             | 4 98         | 6.3            | 605       | Н  | US-08-190- | -            | , Applicati  | -         |
| -•            | 5 95         | 6.1            | 912       | -  | us-01-189- | Sequence 8,  | Applicatio   | 4         |
|               | 6 95         | 6.1            | 912       | Н  | US-08-487- | -            | Applicatio   | 2.37e+01  |
| -             | 7 95         | 6.1            | 912       | Н  | us-08-005- |              | Applicatio   | 2.37e+01  |
|               | 8 94         | 6.1            | 4472      | ~  | US-08-804- |              | Applicatio   | 2.75e+01  |
|               | 6            | 0.9            | 405       | ო  | PCT-US93-1 | Sequence 2,  | Applicatio   | 3.18e+01  |
| Ä             | 0 92         | 5.9            | 681       | ~  | US-08-346- | Sequence 37  | ', Applicati | 3.69e+01  |
| ri            | 1 92         | 5.9            | 681       | н  | us-08-083- | Sequence 18  | 3, Applicati | 3.69e+01  |
| 4             | 2 92         | 5.9            | 1078      | Н  | US-08-083- | Sequence 11  | l, Applicati | 3.69e+01  |
| -             | 3 92         | 5.9            | 1078      | ~  | US-08-346- | Sequence 32  | 2, Applicati | 3.69e+01  |
| Ä             | 4 92         | 5.9            | 1078      | ч  | US-08-465- | Sequence 32  | 2, Applicati | 3.69e+01  |
| ٦.            | 5 92         | 5.9            | 1078      | Н  | US-08-264- | Sequence 32  | 2, Applicati | 3.69e+01  |
| 7             | 6 92         | 5.9            | 2544      | ~  | ns-08-576- | Sequence 32  | 2, Applicati | 3.69e+01  |
| 7             |              | υ.<br>0.       | 2556      | ~  | US-08-083- | Sequence 20  | ), Applicati | 3.69e+01  |
| -             |              | 5.7            | 301       | Н  | US-08-420- | Sequence 47  | 7, Applicati | 6.61e+01  |
| 1             | 19 88        | 5.7            | 301       | ~  | US-08-343- | Sequence 22  | 2, Applicati | 6.61e+01  |
|               |              | 5.7            | 1114      | ~  | US-08-576- | Sequence 31  | l, Applicati | 5.71e+01  |
| 2             | 1 87         | 5.6            | 122       | ~  | US-08-475- | Sequence 19  | 9, Applicati | 7.63e+01  |
| 7             | 2 87         | 5.6            | 122       | Н  | US-08-476- | Sequence 19  | Applicati    | 7.63e+01  |
| 7             | 3 87         | 5.6            | 122       | Н  | US-07-956- | Sequence 19  | 9, Applicati | 7.63e+01  |
|               |              |                |           |    |            |              |              |           |

| 87 5.6 122 1 US-08-485- Sequence 19, Applicating 7.63e+01 85 5.5 365 2 US-08-481- Sequence 2, Applicating 7.63e+01 85 5.5 379 1 US-08-423- Sequence 2, Applicating 1.02e+02 85 5.5 379 1 US-08-444- Sequence 2, Applicating 1.02e+02 85 5.5 379 1 US-08-347- Sequence 2, Application 1.02e+02 85 5.5 379 3 PCT-US95-0 Sequence 2, Application 1.02e+02 85 5.5 379 3 PCT-US95-0 Sequence 2, Application 1.02e+02 85 5.5 379 3 PCT-US95-0 Sequence 2, Application 1.02e+02 86 5.5 379 3 PCT-US95-0 Sequence 3, Application 1.02e+02 86 5.5 379 3 PCT-US95-1 Sequence 3, Application 1.02e+02 86 5.5 393 1 US-08-423- Sequence 11, Application 8.81e+01 86 5.5 2254 2 US-08-677- Sequence 2, Application 8.81e+01 86 5.5 2254 2 US-08-677- Sequence 3, Application 8.81e+01 86 5.5 2550 1 US-08-329- Sequence 6, Application 8.81e+01 US-08-328- Sequence 6, Application 8.81e+01 US-08-328- Sequence 11, Application 1.02e+02 US-08-328- Sequence 11, Appli | ce 3, Application US/ nce 3, Application US/ nce 3, Application US/ two. 5830660 ELCANT: Hillman, Je PLICANT: Hillman, Je PLICANT: Goll, Surya TLE OF INVERTION: OMBER OF SEQUENCES: 3 RRESPONDENCES: 3 RRESPONDENCES: 3 RRESPONDENCES: 3 RRESPONDENCES: 3 RRESPONDENCES: 3 RRESPONDENCES: 3 STATE: CA COUNTRY: DSA ZIP: Palo Alto STATE: CA COUNTRY: DSA ZIP: PA10 ALTO COPERATION SYSTEM: DSA ZIP: PA10 ALTO COPERATION SYSTEM: DSA MEDIUM TYPE: Diskett COMPUTER: EACASIE FORM: MEDIUM TYPE: Diskett COMPUTER: EACASIE COMPUTER: EACASIE COMPUTER: BENEVAL MEDIUM TYPE: DISKET COMPUTER: BENEVAL MEDIUM TYPE: DISKET CLEASIFICATION NUMBER: TORNEY/AGENT INFORMAT REPERRENCE/POCKET NUMBER: FILING DATE: TORNEY/AGENT INFORMAT REPERRENCE/POCKET NUMBER: FELECOMMUNICATION INFORMAT TELECOMMUNICATION INFORMAT TELECOMMUNICATION OF SEQ ID NO COURTED CHARACTERISTIC LECOMMUNICATION FOR SEQ ID NO COURTED CHARACTERISTIC LENGTH: 195 amino acid                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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| 4U0V000H0W4W0V000H0W4U                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | XXXXXX  XXXXXX  SCORPTED STATE  APPLICATION OF STATE  CONTRIBUTION OF STATE  APPLICATION |
| 44444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ### ##################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

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 98 ELFCTEYQNNKNSLETLLGSIGRSLPHITDVSWRLEYQIKTNQLHKMYRPGYLVTLNVEN 157
 Gaps
 4;
 Score 124; DB 2; Length 195;
Pred. No. 2.71e-01;
33; Mismatches 37; Indels
 Sequence 1, Application US/08822260
Patent No. 5830660
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TILLE OF INVENTION: NOVEL TUMORIGENESIS PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDESS: 3
CORRESPONDESSE: Incyte Pharmaceuticals, Inc.
 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,260
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 195 AA
 158 NDSQSYPEINFSCNMEQLQDLVG-KLKDASKSLER 191
 ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0247 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 265569
IENCE 195 AA; 22037 MW; 190094 CN;
 LIBRARY: UTRSNOT02
CLONE: 2267574
VCE 195 AA; 22151 MW; 196728 CN;
 PRT;
 Sequence 1, Application US/08822260
 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
 LENGTH: 195 amino acids
TYPE: amino acid
STRANDEDNESS: single
 STANDARD;
 Best Local Similarity 22.1%;
Matches 21; Conservative
 TOPOLOGY: linear IMMEDIATE SOURCE:
 STREET: 3174 POI
CITY: Palo Alto
STATE: CA
 USA
 FILING DATE:
 ZIP: 94304
 T 2
US-08-822-260-1
 COUNTRY:
 SEQUENCE
 Query Match
 SEQUENCE
 XXXXXX
 RESULT
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Query Match 6.7%; Score 104; DB 1; Length 603;
Best Local Similarity 31.9%; Pred. No. 6.12e+00;
Matches 38; Conservative 31; Mismatches 36; Indels 14; Gaps 13;
 98 ELFCTEYQNNKNSLEILLGSIGRSLPHITDVSWRLEYQIKTNQLHRMYRPAYLVTLSVQN 157
 272 DLSHNRVAGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGE 331
 Gaps
 4;
 Sequence 50, Application US/08190802A
Patent No. 551903
GENERAL INFORMATION
BEDELICANT: Mochly Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
ICE 603 AA; 66811 MW; 1806049 CN;
 Length 195;
Score 118; DB 2; Length 195
Pred. No. 7.00e-01;
29; Mismatches 40; Indels
 SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: U1-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGBNT INFORMATION:
NAME: Fabian, Gary R.
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
 603 AA.
 158 TDSPSYPEISFSCSMEQLQDLVG-KLKDASKSLER 191
 ADDRESSEE: Dehlinger & Associates STREET: P.O. Box 60850 CITY: Palo Alto STATE: CA
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 50, Application US/08190802A
 TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID 00: 50: SEQUENCE CHARACTERISTICS:
 STANDARD;
 : 603 amino acids
amino acid
 COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
Query Match
Best Local Similarity 23.2%;
Matches 22; Conservative
 TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 HYPOTHETICAL: N
ANTI-SENSE: NO
 US-08-190-802A-50
 SECUENCE
 XXXXXX
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RESULT 5
ID US-07-789-915A-8
 TOPOLOGY:
 SEQUENCE
 XXXXX
 XXXXXX
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 76 NLSEERLAVLLAGT-HTLLQ-QALRLP--P-ASLKPDAFQE-E-LQELGIPQDLIGDLAS 128
 272 DLSHNRVAGLLEDTFPGLLGLRVLRLSHNAIASLRPRTFKDLHFLEELQLGHNRIRQLAE 331
 332 RIFEGLGQLEVL-TLNDNQITEV-RVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKL 388
 7; Gaps
 ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
UENCE 605 AA; 66034 MW; 1699376 CN;
 Sequence 49, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
 15; Mismatches 17; Indels
 Query Match 6.3%; Score 98; DB 1; Length 605; Best Local Similarity 38.1%; Pred. No. 1.51e+01; Matches 24; Conservative 15; Mismatches 17; Indels
 COMPUTE TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
 605 AA.
 8600-0139
 PRT;
 ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
 Sequence 49, Application US/08190802A
 ATTORNEY FACENT INFORMATION:
NAME: Fabian, Gary R.
REGISTATION UNDRER: 33,875
REFERENCE/DOCKET UNDRER: 8600-
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 49:
 STANDARD;
 SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acid
TYPE: amino acid
 TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 TRY: USA
94306-0850
 RESULT 4
ID US-08-190-802A-49
 COUNTRY:
 332 RSF 334
 LAF 131
 SEQUENCE
 XXXXXX
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Gaps
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 GENERAL INFORMATION:
APPLICANT: Baker, Rohan T.
APPLICANT: Toblas, John W.
APPLICANT: Warshavsky, Alexander
TITLE OF INVENTION: Ubquitin-Specific Proteases
CORRESPONDENCE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STRATE: Massachusetts
COUNTRY: U.S.A.
 Query Match 6.1%; Score 95; DB 1; Length 912; Best Local Similarity 31.1%; Pred. No. 2.37e+01; Matches 14; Conservative 16; Mismatches 15; Indels
 CURRENT APLICATION NUMBER: DC-DOS/MS-DOS
CURRENT APLICATION DATA:
APPLICATION NUMBER: US/07/789,915A
CLASSIFCATION: 435
TTORNEY/APPLICATION: 435
 705 FRSVLDIPNNKESQSITLDPFQTIQLDISDAGVNDLETAFKKFSE 749
 Sequence 8, Application US/08487203A
Patent No. 5683904
GENERAL INFORMATION:
APPLICANT: Baker, Rohan T.
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
APPLICANT: Valexander
TITLE OF INVENTION: Ubiquitin-Specific Proteases
 912
 MOLECULE TYPE: protein
ENCE 912 AA; 101916 MW; 4327836 CN;
PRT;
 PRT;
 ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 8, Application US/07789915A Patent No. 5212058
 Sequence 8, Application US/07789915A
 Sequence 8, Application US/08487203A
 ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
 22,592
 LENGTH: 912 amino acids TYPE: AMINO ACID
STANDARD;
 STANDARD;
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 617-861-9540
 linear
 US-08-487-203A-8
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 Query Match 6.1%; Score 95; DB 1; Length 912;
Best Local Similarity 31.1%; Pred. No. 2.37e+01;
Matches 14; Conservative 16; Mismatches 15; Indels
 Sequence 2, Application US/08804227C

Sequence 2, Application US/08804227C

Patent No. 587691

GENERAL INFORMATION:
APPLICANT: Behoff, Bradley S.
APPLICANT: Kuhatoss, Stuart A.
APPLICANT: Kuhatoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
ITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STREET: UN
 705 FRSVLDIPNNKESQSITLDPFQTIQLDISDAGVNDLETAFKKFSE 749
 4472 AA.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/005,002C
FILING DATE: 15-JAN-1993
CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08 07/789,915
FILING DATE: 08-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: FAITEL! Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-5091AAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207-363-0558
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CARACTERISTICS:
LENGTH: 912 amino acids
FILENGER AND ACIDS COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: ASCITOOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/POCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: protein
ENCE 912 AA; 101916 MW; 4327836 CN;
 PRT;
 ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 STANDARD;
 TOPOLOGY: linear
 US-08-804-227C-2
 SEQUENCE
 XXXXXX
 RESULT
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 Gaps
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 Query Match 6.1%; Score 95; DB 1; Length 912; Best Local Similarity 31.1%; Pred. No. 2.37e+01; Matches 14; Conservative 16; Mismatches 15: Tindele
 Sequence 8, Application US/08005002C
Patent No. 5494818
GENERAL INFORMATION:
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: Ubjquitin-Specific Proteases
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: Maine
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBP C COMPAILLE
COMPUTER: DATENTIN Release #1.0, Version #1.25
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,203A
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAMME: FATTEAL! Kevin M.
REGISTRATION NUMBER: MIT-5091A3Z
TELEPHONE: 207-363-0558
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 912 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: ACTURED TO THORNEY ACTURED TO THE ACTURED TO
 705 FRSVLDIPNNKESQSITLDPFQTIQLDISDAGVNDLETAFKKFSE 749
 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Revin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: YOYE Harbor
STATE: Maine
COUNTRY: U.S.A.
 MOLECULE TYPE: protein
FENCE 912 AA; 101916 MW; 4327836 CN;
 PRT;
 Sequence 8, Application US/08005002C
 STANDARD;
 03911
 RESULT 7
ID US-08-005-002C-8
 SEQUENCE
 XXXXXX
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Gaps

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 Score 94; DB 2; Length 4472;
Pred. No. 2.75e+01;
42; Mismatches 59; Indels 13; Gaps 10;
 4287 GGAPAPAGGEGTAERLAGLGEEARLRELVRLVRAEVSGVLGYSGPDAVEPGRPFKDLGFD 4346
 4347 SLTAVELRNRLGAATGLRLPTALVFDRPTSQAVAEYLAAELAGPRD-GGDTAAAAFEGLE 4405
 Sequence 2, Application PC/TUS9311404
GENERAL INFORMATION:
APPLICANT: THE BOARD OF TRUSTEES OF LELAND STANFORD
APPLICANT: JUNIOR UNIVERSITY
TITLE OF INVENTION: MUCCGAL VASCULAR ADDRESSIN, DNA AND
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 2
 Score 93; DB 3; Length 405;
Pred. No. 3.18e+01;
20; Mismatches 13; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: FP-57452/BIR;STAN-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 405 AA
 4406 ALAAAVGALAEDDLRR-DVLRRRLTELAAALTPQGRN 4441
 MOLECULE TYPE: protein
JENCE 4472 AA, 463281 MW; 93208012 CN;
 APPLICATION NUMBER: PCT/US93/11404
FILING DATE: 23-Nov-1993
 PRT;
 MOLECULE TYPE: protein
SEQUENCE 405 AA; 43651 MW; 918196 CN;
 Sequence 2, Application PC/TUS9311404
 CORRESPONDENCE ADDRESS:
ADDRESSE: Bertram I. Rowland
STREET: 4 Embarcadero Center
CITY: San Francisco
STATE: California
COUNTRY: USA
 4472 amino acids
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 405 amino acids TYPE: amino acid
 STANDARD;
 ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 / Match 6.1%;
Local Similarity 27.4%;
nes 43; Conservative
 Query Match 6.0%;
Best Local Similarity 31.6%;
Matches 18; Conservative
 TOPOLOGY: unknown
 amino acid
 linear
 CLASSIFICATION:
 JT 9
PCT-US93-11404-2
 TOPOLOGY:
LENGTH:
 SEQUENCE
 Query Match
 XXXXXX
 Matches
 RESULT
 888888
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Gaps

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Sequence 37, Application US/08346128
Patent No. 585641
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
 486 MVGPLHSSLAASALSQMMSYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQ 545
 :||:||:
55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
 Gaps
168 EEIQEAEGTPLFRMTQ-RWRLP-SLGTPAPP-ALHCQVTMQLPKLV--LTHRKEIPV 219
 3,
 Score 92; DB 2; Length 681;
Pred. No. 3.69e+01;
15; Mismatches 29; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,128
 681 AA.
 Ş
 681
 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIIY: New York
 PRT;
 TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE 681 AA; 71840 MW; 2534721 CN;
 PRT;
 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879,038
FILLING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
 Sequence 37, Application US/08346128
 REFERENCE, DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEFAN: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
 STANDARD;
 STANDARD;
 unknown
 Query Match 5.9%;
Best Local Similarity 29.9%;
Matches 20; Conservative
 amino acid
 STATE: New York COUNTRY: U.S.A. ZIP: 10036
 STRANDEDNESS:
 FILING DATE:
 T 11
US-08-083-590A-18
 US-08-346-128-37
 546 -QSLOPP 551
 113 LOELGIP 119
 LENGIH:
 RESULT
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US-09-223-796-2.rai

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APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
 Sequence 32, Application US/08346128

Patent No. 5856441

GENERAL INFORMATION:
APPLICANT: Artavanis-TEAKonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
 893 MVGPLHSSLAASALSQMMSYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQ 952
 Score 92; DB 1; Length 1078;
Pred. No. 3.69e+01;
15; Mismatches 29; Indels 3; Gaps
 MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
COMPUTER: IBM PC compatible
CORFWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/083,590A
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
ATONEY/AGENT INFORMATION:
NAME: MISSIOCK, S. Leslie
REGISTRATION NUMBER: 18,872
 1078 AA.
 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTR: U.S.A.
 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
 MOLECULE TYPE: protein
JENCE 1078 AA; 116254 MW; 5971068 CN;
 REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
 Sequence 32, Application US/08346128
 STANDARD;
 COMPUTER READABLE FORM:
 Query Match 5.9%;
Best Local Similarity 29.9%;
Matches 20; Conservative
 unknown
 TYPE: amino acid
TOPOLOGY: unknown
 CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
 JT 13
US-08-346-128-32
 953 -QSLQPP 958
 113 LQELGIP 119
 SEQUENCE
 XXXXXX
 RESULT
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 Sequence 18, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:
APPLICANT: Attavan1s-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
 486 MVGPLHSSLAASALSOMMSYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQ 545
 Gaps
 .;
e
 MEDIUM TYPE: CIPOPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OFFWARE: Patentin Release #1.0, Version #1.25
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-JUN-1993
CLASSITEATION NUMBER: 135
ATORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Lealie
REGISTRATION NUMBER: 7326-015
TELEPHOKE/DOCKET NUMBER: 7326-015
TELEPHOKE/DOCKET NUMBER: 7326-015
TELEPHOKE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEPHOKE: 641 PENNIE
INFORMATION FOR SEO ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 mm.no acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: unknown
 Query Match 5.9%; Score 92; DB 1; Length 681; Best Local Similarity 29.9%; Pred. No. 3.69e+01; Matches 20; Conservative 15; Mismatches 29; Indels
 1078 AA.
 PRT;
 MOLECULE TYPE: peptide
JENCE 681 AA; 71840 MW; 2534721 CN;
 Sequence 11, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:
 Sequence 11, Application US/08083590A
 Sequence 18, Application US/08083590A
 STANDARD;
 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
 r 12
US-08-083-590A-11
 113 LOELGIP 119
 546 -QSLQPP 551
 SEQUENCE
 XXXXXX
 RESULT
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REFERENCE/DOCKET NUMBER: 7326-004
 T 15
US-08-264-534-32
 953 -QSLQPP 958
 113 LQELGIP 119
 Query Match
 XXXXXX
 Matches
 RESULT
ID US
 8888888888888888888888888
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 ģ
 Sequence 32, Application US/08465500

Patent No. 5789195

GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Muskavitch, Marc A.T.
APPLICANT: Rebay, Ilaria
APPLICANT: Rebay, Ilaria
APPLICANT: Blaumueller, Cristine M.
APPLICANT: Shepard, Scott B.
TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 34
 893 MYGPLHSSLAASALSQMMSYQGLPSTRLATQPHLYQTQQYQPQNLQMQQQNLQPANIQQQ 952
 Score 92; DB 2; Length 1078;
Pred. No. 3.69e+01;
15; Mismatches 29; Indels 3; Gaps
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,128
 1078 AA.
 STREET: 1155 Avenue of the Americas CITY: New York
 TOPOLOGY: unknown
MOLECULE TYPE: protein
FENCE 1078 AA; 116254 MW; 5971068 CN;
 18,872
7326-009
 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879,038
FILING DATE: 30-ARR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MISTORY, S. LESLIE
REGISTRATION NUMBER: 18,72
REFERENCE/DOCKET NUMBER: 7326-009
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELERAX: 212 869864/9741
TELERAX: 212 RENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
 PRT;
 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 32, Application US/08465500
 STANDARD;
 / Match
Local Similarity 29.9%;
les 20; Conservative
 CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE &
 amino acid
 FILING DATE:
 JT 14
US-08-465-500-32
 953 -QSLQPP 958
 113 LQELGIP 119
 SEQUENCE
 Query Match
 XXXXXX
 Matches
 RESULT
888888888888888888888888888888888
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Sequence 32, Application US/08264534
Patent No. 5648464
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
 893 MVGPLHSSLAASALSQMMSYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPANIQQQ 952
 55 VVGALHGKDCREAVEQLGASANLSEERLAVL--LAGTHTLLQQALRLPPASLKPDAFQEE 112
 3,
 Length 1078;
 Score 92; DB 1; Length 1078
Pred. No. 3.69e+01;
15; Mismatches 29; Indels
 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 1078 AA
 CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
 ., v
05-JUN-1995
NN: 435
 TOPOLOGY: unknown MOLECULE TYPE: protein SEQUENCE 1078 AA; 116254 MW; 5971068 CN;
 7326-034
 PRT;
 CURRENT AFFLACATION NUMBER: US/08/465,50
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-0:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 799-9090
TELEFAX: (212) 799-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 anino acids
 Sequence 32, Application US/08264534
 18,872
 STANDARD;
 ESS: single
unknown
 / Match 5.9%;
Local Similarity 29.9%;
nes 20; Conservative
 LENGTH: 1078 amino
TYPE: amino acid
STRANDEDNESS: sing
 CITY: New York
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Search completed: Fri May 12 10:28:29 2000 Job time : 22 secs.

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| ******                                  |      | ****                                     |
| ******                                  |      | *****                                    |
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| ******                                  |      | *******                                  |
| ******                                  |      | ******                                   |
| *                                       |      | * *                                      |

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri May 12 10:27:14 2000; MasPar time 29.86 Seconds 177.710 Million cell updates/sec MPsrch\_pp Run on:

Tabular output not generated.

>US-09-223-796-2 (1-224) from US09223796.pep 1552 1 MSALGAAAPYLHHPADSHSG......ALVLKEMAELEKKCERKLQD 224 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq36 1:geneseqp Database:

Mean 32.859; Variance 162.439; scale 0.202 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|               |       | æ     |        |    | COLUMNICO |                        |           |
|---------------|-------|-------|--------|----|-----------|------------------------|-----------|
| Result<br>No. | Score | Query | Length | DB | 01        | Description            | Pred. No. |
| H             | 1552  | 100.0 | 224    | -  | W37723    | Rat Hypertension relat | 2.90e-120 |
| 7             | 119   | 7.7   | 169    | ~1 | W88390    | Human Zneul partial po | 1.446+00  |
| ٣             | 119   | 7.7   | 181    | -  | W88391    | Zneul partial          | 1.44e+00  |
| 4             | 119   | 7.7   | 254    | -  | W88382    | 44                     | 1.446+00  |
| 2             | 119   | 7.7   | 273    | 1  | W88381    |                        | 1.44e+00  |
| 9             | 118   | 7.6   | 195    | Ч  | W71684    | acid sequence          | 1.69e+00  |
| 7             | 118   | 7.6   | 196    | Н  | X07867    | Human secreted protein |           |
| 80            | 104   | 6.7   | 603    | -  | R85889    |                        | 1.46e+01  |
| σ             | 103   | 9.9   | 262    | Н  | R42079    | G)                     | 1.69e+01  |
| 10            | 86    | 6.3   | 605    | Н  | R85888    | WD-40 domain-contq. in | 3.57e+01  |
| 11            | 97    | 6.2   | 178    | Н  | W95014    | Chicken MGF sequence.  | 4.14e+01  |
| 12            | 95    | 6.1   | 912    | Н  | R36731    | Ubiquitin-specific pro | 5.56e+01  |
| 13            | 94    | 6.1   | 4472   | Н  | W22601    | Tylactone synthase ORF | 6.43e+01  |
| 14            | 93    | 6.0   | 166    | ч  | W05049    | Human thrombopoletin d | 7.44e+01  |
| 15            | 93    | 9.0   | 405    | М  | R57140    | Mouse mucosal addressi | 7.44e+01  |
| 16            | 93    | 6.0   |        | ٦  | W60615    | Mouse mucosal adressin | 7.44e+01  |
| 17            | 93    | 6.0   |        | Н  | R26189    | Epidemic NANBH virus a | 7.44e+01  |
| 18            | 91    | 5.9   | 193    | Н  | W14142    | Erythropoietin variant | 9.95e+01  |
| 19            | 91    | 5.9   | 390    | -  | W97585    | An ACI-1 polypeptide.  | 9.95e+01  |
| 20            | 91    | 5.9   | 920    | Н  | W82500    | Human OGT protein.     | 9.95e+01  |
| 21            | 91    | 5.9   | 1078   | Н  | R28963    | Notch hN3k full length | 9.95e+01  |
| 22            | 90    | 5.8   | 196    | Н  | R84618    | Oilseed rape acetyl Co | 1.15e+02  |
| 23            | 88    | 5.7   | 332    | ч  | R99525    | Neutral protease of Cl | 1.33e+02  |

| 1.53e+02 | 1.53e+02               | 1.33e+02               | 1.33e+02               | 1.53e+02               | 1.33e+02               | 1.33e + 02             | 1.53e+02               | 1.76e+02               | 1.76e+02               | 1.76e+02               | 1.76e+02               | 1.76e+02               | 1.76e+02        | 1.76e+02              | 2.03e+02               | 2.03e+02              | 2.03e+02               | 2.03e+02               | 2.03e+02               | 2.03e+02 | 2.03e+02               |
|----------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------------|-----------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|----------|------------------------|
|          | Amino acid of the spec | Sugar biosynthesis enz | S.erythraea dTDP-4-ket | Thermococcus celer pho | Maize nitrite reductas | Rhodopseudomonas sp. p | Adenylate cyclase prot | Leishmania antigen Lmg | EPO encoded by clone i | Mpl ligand analogue, [ | Secreted protein encod | H. pylori inner membra | Human Factor V. | Deduced from Lelystad | Human erythropoietin a | Pineal gland specific | Mitogen activated prot | Mitogen activated prot | GST-INL fusion interna | ACCase.  | Human mitosin amino ac |
| W12929   | W60244                 | W19734                 | W99387                 | W42391                 | R12517                 | W06719                 | W64518                 | W70228                 | P50343                 | W12928                 | W88549                 | W20991                 | W04254          | R29939                | R71211                 | W09405                | W32868                 | W32867                 | R93270                 | R76949   | W23996                 |
| н,       | -                      | Н                      | Н                      | Н                      | Н                      | Н                      | Н                      | Н                      | Н                      | Ч                      | н                      | Н                      | Н               | Н                     | Н                      | Н                     | Н                      | Н                      | ч                      | ч        | -                      |
| 332      | 320                    | 360                    | 361                    | 440                    | 267                    | 936                    | 1874                   | 169                    | 193                    | 332                    | 548                    | 614                    | 2224            | 2396                  | 166                    | 345                   | 368                    | 393                    | 746                    | 2254     | 2482                   |
| 5.7      | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.7                    | 5.6                    | 5.6                    | 5.6                    | 5.6                    | 5.6                    | 5.6             | 5.6                   | 5.5                    | 5.5                   | 5.5                    | 5.5                    | 5.5                    | 5.5      | 5.5                    |
| 88       | 80                     | 83                     | 83                     | 88                     | 88                     | 83                     | 88                     | 87                     | 87                     | 87                     | 87                     | 87                     | 87              | 87                    | 98                     | 98                    | 86                     | 86                     | 98                     | 98       | 86                     |
| 24       | 25                     | 56                     | 27                     | 28                     | 29                     | 30                     | 31                     | 32                     | 33                     | 34                     | 35                     | 36                     | 37              | 38                    | 39                     | 40                    | 41                     | 42                     | 43                     | 44       | 45                     |

| ALIGNMENTS | itan<br>111111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Ouery Match 100.0%; Score 1552; DB 1; Length 224; Best Local Similarity 100.0%; Pred. No. 2.90e-120; Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 1 MSALGAAAPYLHHPADSHSGRVSFLGSQPSPEVTAVAQLLKDLDRSTFRKLLKLVVGALH 60<br> |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|
|            | W3723 standard W3723 standard W37723 (f Rat Hypertension re extracteluar re Extracteluar cancer; inflamm Rattus rattus. Key MSC_difference W09749807-A2. 31-DEC-1997. 23-UNN-1996; US (GOSS) GOSSARD (HAMET) HAMET P (LEWA) LEWANCZ (TREW) TREMBIA GOSSARD ( | Ouery Match<br>Best Local Simi<br>Matches 224;                                                                                                                    | 1 MSALGAA<br>       <br>1 MSALGAA                                     |
|            | CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | O M. W                                                                                                                                                            | oy ob                                                                 |

61 GKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQ 120

<del>a</del>

e.g. treat Alzheimer's

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This claimed polypetide comprises amino acid residues 1-85 and 159-234 of the human Zneul mature protein (see W88382). i.e. the first HSMHG3W5a homology domain fused to the second HSMHG3W5a homology domain of Zneul. Is a new neuro-growth factor-like homology domain of Zneul is a new neuro-growth factor-like protein that can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. Zneul may also play a role in breast to treat Alzheimer's disease, cancer, or epopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed Earlility and contraception, or to regenerate nerves. Claimed Earlility and contraception, or to regenerate nerves. Claimed Sneul polypeptides (see also W8882-97), including specific domains of Zneul and epitope-bearing portions of Zneul, can be used to
 New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells claim 6; Pege 48-49; 70pp; English.

This polypeptide comprises human Zneul mature polypeptide. Zneul is a new neuro-growth factor-like protein (see also W88381). Its closest human homologue is HSMC3W5A, a gene in the HLA class III region, which is contained in a cosmid which contains Notch 4. Zneul is also homologous to Notch 4 in its EGF-like domains and may
 W88382;
26-APR-1999 (first entry)
Human neuro-growth factor-like protein; human; breast cancer;
Zneu-li neuro-growth factor-like protein; human; breast cancer;
glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
nerve regeneration; haematopolesis; fertility; contraception;
 /note= "hydrophilic domain (HSM1), homologous to
 /note= "domain HSM2 homologous to an HSMHC3W5A
 "epidermal growth factor-like domain 1"
 "epidermal growth factor-like domain 2"
 raise specific antibodies for use e.g. in diagnostic assays
 105 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQ 154
 Score 119; DB 1; Length 181
Pred. No. 1.44e+00;
13; Mismatches 13; Indels
 (ZYMO) ZYMOGENETICS INC.
Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO,
Whitmore TE;
 (ZYMO) ZYMOGENETICS INC.
Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO,
Whitmore TE;
 New mammallan Zneul polypeptides - used to, e. disease, cancer and to repopulate blood cells Claim 6; Page 58; 70pp; English.
 an HSMHC3W5A domain
 Location/Qualiflers
 W88382 standard; Protein; 254 AA.
 er
.158
/note= "ep'
 Match 7.7%;
Local Similarity 42.0%;
les 21; Conservative
 .116
 23-DEC-1998.
18-JUN-1998; U12763.
18-JUN-1997; US-878322.
18-JUN-1997; US-050143.
 /note=
 WPI; 99-095324/08.
 WPI: 99-095324/08
 18-JUN-1997;
18-JUN-1997;
 WO9857983-A2.
 Homo sapiens.
 Sequence
 Query Match
 Domain
 Domain
 Doma1n
 Domain
Domain
 Best Loca
Matches
 RESULT
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 the human zneul mature protein (see also W88382), i.e. the 2 epidermal court factor-like domains (see also W88382), i.e. the 2 epidermal corwth factor-like domains (see also W88384-85) and the second HSMHG3M2A homology domain of zneul. Zneul is a new neuro-growth factor-like protein that can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, chivroid and lymph nodes. Zneul may also play a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul can be used to treat Alzheimer's disease, cancer, to repopulate blood cells of after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed zneul polypeptides (see also W88382-97), including specific domains of zneul and epitope-bearing portions of zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.
 GKDCREAVEQLGASANLSEERLAVLLAGTHTLLQQALRLPPASLKPDAFQEELQELGIPQ 120
 DLIGDLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQL 180
 New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells. Claim 6; Page 57-58; 70pp: English. This claimed polypeptide comprises amino acid residues 105-273 of
glioblastoma; pituitary adenoma; Alzheimer's disease; therapy; nerve regeneration; haematopolesis; fertility; contraception; antibody.
 W88391;
26-APR-1999 (first entry)
Human Sneul partial polypeptide.
Zneul partial polypeptide.
Zneul; neuro-growth factor-like protein; human; breast cancer; glioblastoma; pituitary adenoma; Alzheimer's disease; therapy; nerve regeneration; haematopoiesis; fertility; contraception;
 Score 119; DB 1; Length 169;
Pred. No. 1.44e+00;
13; Mismatches 13; Indels 3;
 93 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQ 142
 181 KLIDGSAHRFEVPIAKFQELRYSVALVLKEMAELEKKCERKLQD 224
 Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO,
 .r 2
W88390 standard; Protein; 169 AA.
 26-APR-1999 (first entry)
uman Zneul partial polypeptide.
Zneu-1; neuro-growth factor-like
9lioblastoma; pituitary adenoma.
 T 3
W88391 standard; Protein; 181 AA.
 Query Match 7.7%;
Best Local Similarity 42.0%;
Matches 21; Conservative
 18-JUN-1998; U12763.
18-JUN-1997; US-878322.
18-JUN-1997; US-050143.
(ZYMO) ZYMOGENETICS INC
 WO9857983-A2.
23-DEC-1998.
18-JUN-1998; U12763.
 Whitmore TE;
WPI; 99-095324/08.
 Homo sapiens.
WO9857983-A2.
 Homo sapiens
 23-DEC-1998
 antibody
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Gaps

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Length 181,

ë,

m

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be involved in BGF receptor pathways. Zneul is widely expressed in adult tissues, with high expression in heart, placenta, spleen, testis, thyroid, spinal cord and lymph node. Zneul can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. It may play a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul may also be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed Zneul polypeptides (see also W88382-97), including specific domains of Zneul and epitope-bearing portions of cancer, can be used to raise specific antibodies for use e.g. in
 New manualian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells

Claim 6; Page 47-48; 70pp; English.

This polypeptide comprises human Zneul, a new neuro-growth factoring polypeptide comprises human Zneul, a new neuro-growth factoring protein. Its amino acid sequence was deduced from the nucleotide sequence (see V84341) of a CDNA clone isolated from a brain cDNA library. Zneul's closest human homologue is HSMRG3N5A, a gene in the HLA class III region, which is contained in a cosmid which contains Notch 4. Zneul is also homologous to Notch 4 in its EGF-like domains and may be involved in EGF receptor pathways.

EGF-like domains and may be involved in some committee of the contain is widely expressed in adult tissues, with high expression in heart, placenta, spleen, testis, thyroid, spinal cond and lymph code. Zneul polypeptide can be used as a growth, maintenance, or
 Gaps
 26-APR-1999 (first entry)
Human neuro-growth factor-like protein Zneul.
Sneul: neuro-growth factor-like protein; human; breast cancer;
glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
nerve regeneration; haematopolesis; fertility; contraception;
 "domain HSM2 homologous to an HSMHC3W5A
 "epidermal growth factor-like domain 1"
 epidermal growth factor-like domain 2"
 ë
 /note= "hydrophilic domain (HSM1), homologous
 178 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQ 227
 DB 1; Length 254;
 Score 119; DB 1; Length 254;
Pred. No. 1.44e+00;
13; Mismatches 13; Indels
 "putative signal peptide"
 Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO,
Whitmore TE;
 an HSMHC3W5A domain
 "mature protein"
 Location/Qualifiers
 W88381 standard; Protein; 273 AA.
 Query Match 7.7%;
Best Local Similarity 42.0%;
Matches 21; Conservative
 136. .177
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178. .273
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 (ZYMO) ZYMOGENETICS INC.
 /note=
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18-JUN-1998; U12763.
18-JUN-1997; US-878322.
18-JUN-1997; US-050143.
 /note=
 'note=
 /note-
 105.
 WPI; 99-095324/08.
N-PSDB; V84341.
 Homo sapiens.
 W09857983-A2
 Seguence
 antibody
 W88381;
 Peptide
 Protein
 Domain
 Domain
 Domain
 Domain
 RESULT
 g
 8888888888888888888
 ò
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```
New tumorigenesis associated protein and related nucleic acid, vectors, transformed cells - antibodies, agonists and antagonists, tor diagnosis, treatment and prevention of abnormal cellular differentiation, particularly cancers and inflammation

To diagnosis, treatment and prevention of abnormal cellular differentiation, particularly cancers and inflammation.

This is the amino acid sequence of the human tumourigenesis associated protein (HTMP), used in the method of the invention. HTMP, constitution acid sequence of the human tumourigenesis associated protein (HTMP), used in the method of the invention. HTMP, is involved with cell proliferation and inflammation. It can be used to stimulate cell proliferation for tumours or infections, or to treat genetic defects). Antagonists of HTMP are used to treat or prevent a wide range of cancers (adenocarcinoms, melanoma, sarroma, lymphoma, cellukaemia etc.), also inflammation where associated with infection or immunological disease (e.g. asthma, cystic fibrosis, rheumatoid arthritis). HTMP is also used to raise antibodies are used as for diagnosis or monitoring of HTMP-related diseases (in usual immonsassys), in competitive drug screens and to isolate HTMP from standard amplification or hybridisation tests to diagnose HTMP-related diseases, to identify related sequences; for genomic mapping and for screen.

Sequence 195 As;
 98 ELFCTEYQNNKNSLEILLGSIGRSLPHITDVSWRLEYQIKTNQLHRMYRPAYLVTLSVQN 157
 125 DLASLAFGSQRPLLDSVAQQQGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQLKLTD 184
 Gaps
 04-DEC-1998 (first entry)
Amino acid sequence of the human tumourigenesis associated protein.
Human, tumourigenesis associated protein, HTAP; transplantation,
tumour, Antagonist, cancer; inflammation; immunological disease;
antibody; probe; primer; PCR; amplification; hybridisation;
 throid and lymph nodes. It may also play a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul may be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed Zneul polypeptides (see also W88382-97), including specific domains of Zneul and epitope-bearing portions of Zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.
differentiation factor in the spinal cord, heart, spleen, testis,
 4;
 ä
 197 KEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQ 246
 Length 273;
 Length 195;
 Score 118; DB 1; Length 195
Pred. No. 1.69e+00;
29; Mismatches 40; Indels
 13; Mismatches 13; Indels
 Score 119; DB 1;
Pred. No. 1.44e+00;
 JT 6
W71684 standard; Protein; 195 AA.
 Query Match
Best Local Similarity 42.0%;
 Query Match 7.6%;
Best Local Similarity 23.2%;
Matches 22; Conservative
 (INCY-) INCYTE PHARM INC. Golf SK, Hillman JL;
 20-MAR-1997; US-822260.
 20-MAR-1998; U06066
 Goli SK, Hillman JI
WPI; 98-521224/44.
 N-PSDB; V5828]
 Homo sapiens.
WO9841635-A1.
 inhibition
 Sequence
 W71684;
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158 TDSPSYPEISFSCSMEQLQDLVG-KLKDASKSLER 191

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06-JUL-1999

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T
R42079 standard; Protein; 262 AA.
603 AA
 Query Match
Best Local Similarity 31.9%;
Matches 38; Conservative
standard; Protein;
 Rattus rattus.
WO9521252-A2.
 Seguence
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Claim 1b; Page 285-286; 368pp; English.

This invention describes novel isolated human genes and the secreted proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides.

Specific uses are described for each of the 101 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, schizophrenia, prostate allergies, Alzhelmer's and cognitive disorders, pulmonary disorders, transplant rejection, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, disease, schizophrenia, osteoporosis, arthritis or malignancies, disease, schizophrenia or cardiae masche disorders, pulmonary disorders, infections and AIDS. The human secreted proteins of the invention are represented in X77852-X07993 and the encoding nucleic acids are represented in X37451-X37552.
 Human secreted protein fragment encoded from gene 16.

Human secreted protein; treatment; prevention; protein therapy; AIDS; gene therapy; daggnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Albinieme's disease; schizophrenia; cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis; arthritis; malignancy; digestive; endocrine; infection.
 ELFCTEYQNNKNSLEILLGSIGRSLPHITDVSWRLEYQIKTNQLHRMYRPAYLVTLSVQN 157
 4
 Length 196;
 Score 118; DB 1; Length 196
Pred. No. 1.69e+00;
29; Mismatches 40; Indels
 Carter KC, Duan DR, Endress GA, Feng P, Ferrie AM, Florence KA, Greene JM, Janat F, Lafleur DW, N1 J, Rosen CA, Ruben SM, Shi Y, Young P, Yu G;
 GSAHRF-EVPIA-KFQELRYSVALVLKEMAE-LEK 216
 158 TDSPSYPEISFSCSMEQLQDLVG-KLKDASKSLER 191
185 GSAHRF-EVPIA-KFQELRYSVALVLKEMAE-LEK
 T
X07867 standard; Protein; 196 AA.
 997; US-060874.
HUMAN GENOME SCI INC.
 Local Similarity 23.2%;
les 22; Conservation
 (first entry)
 01-0CT-1998; U20775.

02-0CT-1997; US-06084.

02-0CT-1997; US-060833.

02-0CT-1997; US-060830.

02-0CT-1997; US-060837.

02-0CT-1997; US-060839.

02-0CT-1997; US-060843.

02-0CT-1997; US-060865.
 99-264022/22.
 N-PSDB; X37466
 Homo sapiens
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02-OCT-1997 (HUMA-) HUM

Query Match Best Loc Matches

125

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98

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185

RESULT

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Score 104; DB 1; Length 603;
Pred. No. 1.46e+01;
31; Mismatches 36; Indels 14; Gaps 13;
13-SEP-1996 (first entry)
WD-40 domain-contg. rat insulin-like growth factor binding protein.
WD04 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein Kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.
 272 DLSHNRVAGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGE 331
 332 RIFEGLGQLEVL-TLNDNQITEV-RVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKL 388
 129 LAF-G-SQRPLLDSVAQQQGSSLPHVSYFRWRVDVAI-STSAQS-RSLQPSVLWQL-KL 182
 Grinsven MQJ;
 WPI; 93-329814/42.
P-PSDB: 049956, 049958.
Recombinant INSV DNA constructs comprising INSV DNA coding for transcription into INSV RNA sequences - are used to transform plants to reduce susceptibility to INSV infection Example 4; Page 44-45; 64Pp; Bng11sh.
INSV RNA was purified from systemically infected Nicotiana rustica
 29-APR-1994 (first entry)
Impatiens Necrotic Spot Virus S nucleocapsid protein.
INSV: tospovirus; resistance; pan-handle secondary structure; plant RNA virus.
Impatiens Necrotic Spot Virus.
EP-566525-A.
 à
 Peters
 20-OCT-1993.
16-MAR-1993: 810190.
19-MAR-1993: 810190.
(SANO) SANDOZ LTD.
(VGRL) VAN GRINSVEN M Q J M.
(SANO) SANDOZ PATENT GABH.
(SANO) SANDOZ -ERFINDUNGEN VERW GES MBH.
(SANO) SANDOZ -ERFINDUNGEN VERW GES WBH.
(SANO) SANDOZ -GABH.
 THE STATE OF THE S
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WO9905280-A1.

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MET. 20 2017 (17.7).

WEW WD-40 (beta-transducin)-derived polypeptide(s) - which alter the activity of a protein, eg. protein kinase C, which interacts with a rotein contg. a WD-40 region.

Example 5; Page 122-125; 351pp; English.

Example 5; Page 122-125; 351pp; English.

Example 5; Page 122-125; 351pp; English.

Proteins R65851-92 are protein which contain at least one WD-40 (also called beta-transducing homologous) amino acid repeat motifs. The WD-40 regions are involved in protein. Protein interactions between proteins funase of involved in intracellular signalling. An example of such an interaction is between protein kinase of and receptors of activated protein kinase (RACK), esp. RACK-1 (R86850). Proteins R85851-82 were isolated based on homology with beta-transducin, whereas proteins R85881-92 were isolated proteins were used to construct the peptides R8423-R85663 and R85786-R85842. The peptides can be used to identify target proteins contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of proteins involved in protein-protein interaction and to screen for drugs contg. And at all affect protein-protein interaction involving WD-40 domains.
 21-MAY-1999 (first entry)
Chicken MGF sequence.
Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
inflammatory condition; drug screening; human; MGF.
Gallus sp.
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 13-529-1996 (first entry)
WD-40 domain-contg. insulin-like growth factor binding protein.
WD-40 domain-contg. insulin-like growth factor binding protein.
WD-40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.
 272 DLSHNRVAGLLEDTFPGLLGLRVLRLSHNAIASLRPRTFKDLHFLEELQLGHNRIRQLAE 331
leaves. The short (S) transcript comprises two genes, one coding for a non-structural protein and the other (on the complementary strand) sequences of the new protein. The 5'- and 3'-terminal sequences of the S RNA are capable of hybridising to each other; the doubble-stranded structure obtained by such hybridisation is referred sequence 262 AA;
 7; Gaps
 Gaps
 Ĥ
 15; Mismatches 17; Indels
 Length 262;
 Length 605;
 Score 103; DB 1; Length 262
Pred. No. 1.69e+01;
12; Mismatches 17; Indels
 137 ATTDLKSCVLGVLLGGSLPLIASVLNFEIAALVPAIYQDAKHVELGI 183
 Score 98; DB 1; L
Pred. No. 3.57e+01;
 10-AUG-1995.
31-JAN-1995; U01210.
01-FEB-1994; US-190802.
(STRD) UNIV LELAND STANFORD JUNIOR.
MOCHLY-ROSEN D. RON D;
WPI; 95-283772/37.
 W95014 standard; peptide; 178 AA.
W95014;
 Z
 T 10
R85888 standard; Protein; 605
 / Match 6.3%;
Local Similarity 38.1%;
hes 24; Conservative
 Query Match 6.6%;
Best Local Similarity 36.2%;
Matches 17; Conservative
 605 AA;
 WO9521252-A2.
 332 RSF 334
 LAF 131
 Sequence
 Query Match
 129
 Matches
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Particular and proposed and proposed processes and proteins. The polynocleotide encoding mammalian cytokine interleukin-B30 (IL-B30), including fragments - useful for requilating activation, development, differentiation and function of various cell types, and for diagnosing and treating conditions a special types, and for diagnosing and treating conditions of processes and conditions and containing a vector comprising the IL-B30 polypeptides. Host cells containing a vector comprising the IL-B30 polypeptides Host cells containing a vector comprising the IL-B30 polypeptides are useful for diagnosis of IL-B30 mediated conditions, and forensic science (e.g. to distinguish rodent from human, or as marker to distinguish between different cells exhibiting differential expression or modification patterns). The IL-B30 including fragments), together with antibodies that bind to IL-B30 are useful for teaching purposes. They are also used for treating conditions associated with abnormal physiclogy or development, including inflammatory conditions. The polypeptide cytokine should mediate cytokine synthesis and proliferation in cells. IL-B30 is useful for drug screening to dentify compounds having binding affinity to IL-B30. The present
 Didutinin-specific protease(s) - specifically cleave fusion proteins regardless of size, at C-terminus of ubiquitin portion claim 13; page 58-64; 78pp; English.

The sequences given in 18729-31 represent the ubiquitin-specific proteases UBP1, UBP2, and UBP3. These proteases specifically cleave the 120 kD fusion protein ubiquitin-methionine-beta-galactosidase (Ub-met-beta-gal) (see also R36728). The proteases UBP1 and UBP2 active in vivo. These proteases have been shown to specifically cleave Ub-met-beta-gal at the C-terminus of the ubiquitin molety. The proteases can be used to deubiquinate fusion proteins in vivo, therefore prokaryotic cells having an expression vector one of these proteases can be further transformed with an expression vector
 encoding a ubiquitin fusion protein. Such cells will then produce a deubiquinated product having a predetermined N-terminal amino acid
 Ubiquitin-specific protease, UBP3.
Fusion protein; ubiquitin-methionine-beta-galactosidase; UBP2; UBP3; expression vector; ubiquitin-specific; protease; UBP1; in vitro; transformation; Ub-met-beta-Gal; in vivo.
 Gaps
 3;
 79 QIRAGLHAYHDSLGAVLRLLPNHTTLVETLQLDAANLSSN-IQQOMEDLGL 128
 Score 97; DB 1; Length 178;
Pred. No. 4.14e+01;
18; Mismatches 13; Indels
 13-MAY-1993.
06-NOV-1992; U09562.
08-NOV-1991; US-789915.
(MASI) MASSACHUSETIS INST TECHNOLOGY.
BAKET RT, TODLAS JW, VALSHAVSKY A;
WPI; 93-167700/20.
 Š
 R36731 standard; Protein; 912
 Query Match 6.2%;
Best Local Similarity 33.3%;
 (first entry)
 Conservative
 US-900905
 SCHERING CORP
 04-FEB-1999.
24-JUL-1998; U15423.
25-JUL-1997; US-9009
 178 AA;
 Bazan JF;
WPI; 99-142935/12.
 N-PSDB; 041290
 26-AUG-1993
 Sequence
 residue
 Matches
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Sequence

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26 GSQPSPEVT-AVAQLLKDL-DRSTFRKLLKLV---VGALHGKDCREAVEQLGASANLSEE 80
 J08168386-A.
 Mus musculus
 Sequence
 peptide
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 DNA encoding Streptomyces fradiae tylactone synthase domain - for production of tylosin-related polyketide compounds claim 9; Pages 66-80; 220pp; English.
W22601-W22605 represent proteins encoded by the tylactone synthase gene cluster of the invention. The gene cluster is also referred to as the tylactone, and was isolated from Streptomyces fradiae. These sequences are multifunctional proteins which direct the synthesis of the polyketide tylactone, isolated from Streptomyces fradiae. Tylactone is the basic modified so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated and/or the post-condensation rections performed, thereby resulting in novel tylosin-related
 ö
 Tylactone synthase ORT1 protein.
Tylactone synthase gene cluster; tylG gene; multifunctional protein;
polyketide; tylactone synthesis; antibiotic; tylosin.
 Gaps
 43. .447
/note= "ketosynthase domain, KSq(s)"
586. .914
/note= "acyltransferase domain, AT(s)"
954. .1038
/note= "acyl carrier protein domain, ACP(s)"
1060. .1483
/note= "ketosynthase domain, KSI"
1060. .1934
/note= "acyltransferase domain, AII"
2199. .2378
 Score 94; DB 1; Length 4472;
Pred. No. 6.43e+01;
42; Mismatches 59; Indels 13;
 ö
 ACP1"
 carrier protein domain, ACP2"
 Length 912;
 Score 95; DB 1; Length 912;
Pred. No. 5.56e+01;
16; Mismatches 15; Indels
 705 FRSVLDIPNNKESQSITLDPFQTIQLDISDAGVNDLETAFKKFSE 749
 "acyl carrier protein domain,
 acyltransferase domain, AT2'
 "ketoreductase domain, KR1"
 "ketoreductase domain, KR2"
 (ELIL) LILLY & CO ELI.
Dehoff BS, Kuhstoss SA, Rosteck PR, Sutton KL;
WPI: 97-418046/39.
 "ketosynthase domain,
 "dehydratase domain,
 'note= "encoded by GTG'
 Location/Qualifiers
 r 13
W22601 standard; Protein; 4472 AA.
 ..etc
...3477
/note= "acyl+
3502.
 6.18;
Query Match 6.1%;
Best Local Similarity 31.1%;
Matches 14; Conservative
 Best Local Similarity 27.4%;
Matches 43; Conservative
 (first entry)
 /note-
2576. .:
 /note-
2469.
 /note-
4016. .
 /note-
4302.
 22-FEB-1996; US-012078.
 /note-
 polyketide; tylactone
Streptomyces fradiae.
 19-FEB-1997; 301056.
 4472 AA;
 Misc_difference
 N-PSDB; T80413
 EP-791655-A2.
 27-FEB-1998
 -AUG-1997
 polyketides
 Sequence
 Query Match
 Domain
 Domain
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Domain
 W22601
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Gaps 10;

4287 GGAPAPAGGEGTAERLAGLGEEARLRELVRLVRAEVSGVLGYSGPDAVEPGRPFKDLGFD 4346

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12;
4347 SLTAVELRNRLGAATGLRLPTALVFDRPTSQAVAEYLAAELAGPRD-GGDTAAARFEGLE 4405
 Thrombopoletin variants having megakaryocyte growth factor, activity useful for promoting growth of megakaryocytes and platelets, also as bloochemical assay reagent
Claim 13: Page 15: 21pp; Japanese.
Four deletion variants of thrombopoletin (TPO), designated dTPO-5, -6, -7 and -8, were engineered. All four variants contained the first 131 residues from the N-terminal region of human TPO and all four variants promoted formation and growth of human megakaryocytes. Proteins comprising at least residues 1-31 of TPO are useful for promoting platelet production. The present sequence is that of dTPO-6 which has the same sequence as wild-type TPO for the first 131 amino acids, followed by residues 319-353 from the C-terminus of
 15 TARLILSSPAPPACDLRVLSKLLRD-SHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGEWK 73
 megakaryocyte;
 74 TOMEETKAQDIL-GAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLLLGALQSL-LGT
 12;
 21-FEB-1995 (first entry)
Mouse mucosal addressin cell adhesion molecule (MAGCAM-1).
Mucosal addressin cell adhesion molecule; MAGCAM-1; leukocyte; endothellum; transmembrane protein; immunoglobulin.
 Length 166;
 56; Indels
 10-DEC-1996 (first entry)
Human thrombopoletin deletion variant dTPO-6.
Human; thrombopoletin; TPO; variant; deletion mutant; megrowth factor; platelet production; thrombocytopolesis.
 4406 ALAAAVGALAEDDLRR-DVLRRRLTELAAALTPQGRN 4441
 Score 93; DB 1; L. Pred. No. 7.44e+01; 38; Mismatches 56
 /note= "transmembrane region"
 /note= "signal peptide"
362. .385
 02-JUL-1996.
13-JUL-1995; 199299.
19-OCT-1994; JP-278657.
(SNOW) SNOW BRAND MILK PROD CO LTD.
WPI; 96-357243/36.
N-PSDB; T41906.
 Location/Qualifiers
 132 QLHPLLPDPSAPTPTPTSPLLNTSY 156
 154
 r 14
WO5049 standard; Protein; 166 AA.
WO5049;
 R57140 standard; Protein; 405 AA. R57140;
 134 Q-RPLL-D-SV-AQQQGSSLPHVSY
 Query Match
Best Local Similarity 26.9%;
Matches 39; Conservative
 166 AA;
 WO9413312-A.
 region
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PF 23-NOV-1993; U11404.

PR 15-DEC-1992; US-990866.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Briskin M, Butcher E;

DR WPI; 94-234206/28.

PY condothelial cells

PY for diagnosis and therapy, e.g. modulating homing of leukocytes of tor diagnosis and therapy, e.g. modulating homing of leukocytes of tor diagnosis and therapy, e.g. modulating homing of leukocytes of tor diagnosis and therapy, e.g. modulating homing of leukocytes of tor diagnosis and therapy, e.g. modulating homing of leukocytes of leukocytes of the modulating has a mucine-like region between the 2nd and 3rd comains, a transmembrane domain and a cytoplasmic domain, where the CC Annalins, a transmembrane domain and a cytoplasmic domain, where the MAd is capable of binding to a leukocyte surface membrane protein.

CC And is capable of binding to a leukocyte surface membrane protein.

CC CONA can be used for screening for molecules capable of binding to protein may be used to treat intestinal inflammatory diseases and autoimmune diseases, and especially intestinal carcinomas, etc.

CC CONA can be used to treat intestinal inflammatory diseases and sequence 405 Ax;

CO Sequence 405 Ax;

CO CONY MATCH SELICEPAPP-ALHCOVTMOLDENLY-LITHREIPY 219

DESTRUCTION OF SELICEPAPP-ALHCOVTMOLDENLY-LITHREIPY 219

1139 DSVAQOGGSSLPHVSYFRWRVDVAISTSAQSRSLQPSVLMQL-KLTDGSAHREEVPI 194
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Search completed: Fri May 12 10:27:49 2000 Job time : 35 secs.

| *        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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